

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: QUENTIN-MILLET, Marie-Jose et al.
- (ii) TITLE OF INVENTION: TBP2 FRAGMENTS OF THE TRANSFERRIN RECEPTOR OF NEISSERIA MENINGITIDIS
- (iii) NUMBER OF SEQUENCES: 42
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: LARSON AND TAYLOR
 - (B) STREET: 727 SOUTH 23RD STREET
 - (C) CITY: ARLINGTON
 - (D) STATE: VIRGINIA
 - (E) COUNTRY: USA
 - (F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/591,447
 - (B) FILING DATE: 29-JAN-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: SARRO, THOMAS P
 - (B) REGISTRATION NUMBER: 19,196
 - (C) REFERENCE/DOCKET NUMBER: XI/P02956
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 703-920-7200
 - (B) TELEFAX: 703-892-8428

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Neisseria meningitidis
 - (B) STRAIN: IM2169

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 60..119

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 120..2192

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 60..2192

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 120..1154

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1155..1748

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1749..2192

(ix) FEATURE:

(A) NAME/KEY: misc_binding
(B) LOCATION: 237..1169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTGTGTTAAA AATAAATAAAA ATAATAATCC TTATCATCTCT TTAATTGAAT TGGGTTTAT 59

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT 107
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
-20 -15 -10 -5

TTG TTG AGT GCC TGT CTG GGC GGC GGC GGC AGT TTC GAT CTT GAT TCT 155
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
1 5 10

GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT 203
Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
15 20 25

TCC GAA AAA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG 251
Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala
30 35 40

ATG AGG TTG AAA CGG AGG AAT TGG TAT CCG GGG GCA GAA GAA AGC GAG 299
Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu
45 50 55 60

GTT AAA CTG AAC GAG AGT GAT TGG GAG GCG ACG GGA TTG CCG ACA AAA	347
Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys	
65 70 75	
CCC AAG GAA CTT CCT AAA CGG CAA AAA TCG GTT ATT GAA AAA GTA GAA	395
Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu	
80 85 90	
ACA GAC GGC GAC AGC GAT ATT TAT TCT TCC CCC TAT CTC ACA CCA TCA	443
Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser	
95 100 105	
AAC CAT CAA AAC GGC AGC GCT GGC AAC GGT GTA AAT CAA CCT AAA AAT	491
Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn	
110 115 120	
CAG GCA ACA GGT CAC GAA AAT TTC CAA TAT GTT TAT TCC GGT TGG TTT	539
Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe	
125 130 135 140	
TAT AAA CAT GCA GCG AGT GAA AAA GAT TTC AGT AAC AAA AAA ATT AAG	587
Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys	
145 150 155	
TCA GGC GAC GAT GGT TAT ATC TTC TAT CAC GGT GAA AAA CCT TCC CGA	635
Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg	
160 165 170	
CAA CTT CCT GCT TCT GGA AAA GTT ATC TAC AAA GGT GTG TGG CAT TTT	683
Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe	
175 180 185	
GTA ACC GAT ACA AAA AAG GGT CAA GAT TTT CGT GAA ATT ATC CAG CCT	731
Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro	
190 195 200	
TCA AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCT GGT GAT GGC AGC	779
Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser	
205 210 215 220	
GAA GAA TAT TCC AAC AAA AAC GAA TCC ACG CTG AAA GAT GAT CAC GAG	827
Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu	
225 230 235	
GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AAT AAG AAA	875
Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys	
240 245 250	
TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AGC CTA AAT AAT AAT ACT	923
Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr	
255 260 265	

B
cont.

AAT Asn 270	AAT Asn 270	GAC Asp	AAA Lys	CAT His	ACC Thr	ACC Thr 275	CAA Gln	TAC Tyr	TAC Tyr	AGC Ser	CTT Leu 280	GAT Asp	GCA Ala	CAA Gln	ATA Ile	971
ACA Thr 285	GGC Gly	AAC Asn	CGC Arg	TTC Phe	AAC Asn 290	GGC Gly	ACG Thr	GCA Ala	ACG Thr	GCA Ala 295	ACT Thr	GAC Asp	AAA Lys	AAA Lys	GAG Glu 300	1019
AAT Asn	GAA Glu	ACC Thr	AAA Lys	CTA Leu 305	CAT His	CCC Pro	TTT Phe	GTT Val	TCC Ser 310	GAC Asp	TCG Ser	TCT Ser	TCT Ser	TTG Leu 315	AGC Ser	1067
GGC Gly	GGC Gly	TTT Phe	TTC Phe 320	GGC Gly	CCG Pro	CAG Gln	GGT Gly	GAG Glu 325	GAA Glu	TTG Leu	GGT Gly	TTC Phe	CGC Arg 330	TTT Phe	TTG Leu	1115
AGC Ser	GAC Asp	GAT Asp 335	CAA Gln	AAA Lys	GTT Val	GCC Ala	GTT Val 340	GTC Val	GGC Gly	AGC Ser	GCG Ala	AAA Lys 345	ACC Thr	AAA Lys	GAC Asp	1163
AAA Lys 350	CTG Leu	GAA Glu	AAT Asn	GGC Gly	GCG Ala	GCG Ala 355	GCT Ala	TCA Ser	GGC Gly	AGC Ser	ACA Thr 360	GGT Gly	GCG Ala	GCA Ala	GCA Ala	1211
TCG Ser 365	GGC Gly	GGT Gly	GCG Ala	GCA Ala	GGC Gly 370	ACG Thr	TCG Ser	TCT Ser	GAA Glu	AAC Asn 375	AGT Ser	AAG Lys	CTG Leu	ACC Thr	ACG Thr 380	1259
GTT Val	TTG Leu	GAT Asp	GCG Ala	GTT Val 385	GAA Glu	TTG Leu	ACA Thr	CTA Leu	AAC Asn 390	GAC Asp	AAG Lys	AAA Lys	ATC Ile	AAA Lys 395	AAT Asn	1307
CTC Leu	GAC Asp	AAC Asn	TTC Phe 400	AGC Ser	AAT Asn	GCC Ala	GCC Ala	CAA Gln 405	CTG Leu	GTT Val	GTC Val	GAC Asp	GGC Gly 410	ATT Ile	ATG Met	1355
ATT Ile	CCG Pro 415	CTC Leu	CTG Leu	CCC Pro	AAG Lys	GAT Asp	TCC Ser 420	GAA Glu	AGC Ser	GGG Gly	AAC Asn	ACT Thr 425	CAG Gln	GCA Ala	GAT Asp	1403
AAA Lys 430	GGT Gly	AAA Lys	AAC Asn	GGC Gly	GGA Gly 435	ACA Thr	GAA Glu	TTT Phe	ACC Thr	CGC Arg 440	AAA Lys	TTT Phe	GAA Glu	CAC His	ACG Thr	1451
CCG Pro 445	GAA Glu	AGT Ser	GAT Asp	AAA Lys	AAA Lys 450	GAC Asp	GCC Ala	CAA Gln	GCA Ala	GGT Gly 455	ACG Thr	CAG Gln	ACG Thr	AAT Asn	GGG Gly 460	1499
GCG Ala	CAA Gln	ACC Thr	GCT Ala	TCA Ser 465	AAT Asn	ACG Thr	GCA Ala	GGT Gly	GAT Asp 470	ACC Thr	AAT Asn	GGC Gly	AAA Lys	ACA Thr 475	AAA Lys	1547

ACC	TAT	GAA	GTC	GAA	GTC	TGC	TGT	TCC	AAC	CTC	AAT	TAT	CTG	AAA	TAC	1595
Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	Leu	Asn	Tyr	Leu	Lys	Tyr	
		480						485					490			
GGA	ATG	TTG	ACG	CGC	AAA	AAC	AGC	AAG	TCC	GCG	ATG	CAG	GCA	GGA	GGA	1643
Gly	Met	Leu	Thr	Arg	Lys	Asn	Ser	Lys	Ser	Ala	Met	Gln	Ala	Gly	Gly	
		495					500					505				
AAC	AGT	AGT	CAA	GCT	GAT	GCT	AAA	ACG	GAA	CAA	GTT	GAA	CAA	AGT	ATG	1691
Asn	Ser	Ser	Gln	Ala	Asp	Ala	Lys	Thr	Glu	Gln	Val	Glu	Gln	Ser	Met	
	510					515					520					
TTC	CTC	CAA	GGC	GAG	CGT	ACC	GAT	GAA	AAA	GAG	ATT	CCA	ACC	GAC	CAA	1739
Phe	Leu	Gln	Gly	Glu	Arg	Thr	Asp	Glu	Lys	Glu	Ile	Pro	Thr	Asp	Gln	
	525				530					535					540	
AAC	GTC	GTT	TAT	CGG	GGG	TCT	TGG	TAC	GGG	CAT	ATT	GCC	AAC	GGC	ACA	1787
Asn	Val	Val	Tyr	Arg	Gly	Ser	Trp	Tyr	Gly	His	Ile	Ala	Asn	Gly	Thr	
				545					550					555		
AGC	TGG	AGC	GGC	AAT	GCT	TCT	GAT	AAA	GAG	GGC	GGC	AAC	AGG	GCG	GAA	1835
Ser	Trp	Ser	Gly	Asn	Ala	Ser	Asp	Lys	Glu	Gly	Gly	Asn	Arg	Ala	Glu	
			560					565					570			
TTT	ACT	GTG	AAT	TTT	GCC	GAT	AAA	AAA	ATT	ACC	GGC	AAG	TTA	ACC	GCT	1883
Phe	Thr	Val	Asn	Phe	Ala	Asp	Lys	Lys	Ile	Thr	Gly	Lys	Leu	Thr	Ala	
		575					580					585				
GAA	AAC	AGG	CAG	GCG	CAA	ACC	TTT	ACC	ATT	GAG	GGA	ATG	ATT	CAG	GGC	1931
Glu	Asn	Arg	Gln	Ala	Gln	Thr	Phe	Thr	Ile	Glu	Gly	Met	Ile	Gln	Gly	
		590				595					600					
AAC	GGC	TTT	GAA	GGT	ACG	GCG	AAA	ACT	GCT	GAG	TCA	GGT	TTT	GAT	CTC	1979
Asn	Gly	Phe	Glu	Gly	Thr	Ala	Lys	Thr	Ala	Glu	Ser	Gly	Phe	Asp	Leu	
	605				610					615					620	
GAT	CAA	AAA	AAT	ACC	ACC	CGC	ACG	CCT	AAG	GCA	TAT	ATC	ACA	GAT	GCC	2027
Asp	Gln	Lys	Asn	Thr	Thr	Arg	Thr	Pro	Lys	Ala	Tyr	Ile	Thr	Asp	Ala	
				625				630						635		
AAG	GTA	AAG	GGC	GGT	TTT	TAC	GGG	CCT	AAA	GCC	GAA	GAG	TTG	GGC	GGA	2075
Lys	Val	Lys	Gly	Gly	Phe	Tyr	Gly	Pro	Lys	Ala	Glu	Glu	Leu	Gly	Gly	
			640					645					650			
TGG	TTT	GCC	TAT	CCG	GGC	GAT	AAA	CAA	ACG	GAA	AAG	GCA	ACA	GCT	ACA	2123
Trp	Phe	Ala	Tyr	Pro	Gly	Asp	Lys	Gln	Thr	Glu	Lys	Ala	Thr	Ala	Thr	
		655					660					665				
TCC	AGC	GAT	GGA	AAT	TCA	GCA	AGC	AGC	GCG	ACC	GTG	GTA	TTC	GGT	GCG	2171
Ser	Ser	Asp	Gly	Asn	Ser	Ala	Ser	Ser	Ala	Thr	Val	Val	Phe	Gly	Ala	
		670				675					680					

6
cont.

AAA CGC CAA CAG CCT GTG CAA TAAGCACGGT TGCCGAACAA TCAAGAATAA
Lys Arg Gln Gln Pro Val Gln
685 690

2222

GGCTTCAG

2230

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
-20 -15 -10 -5

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
1 5 10

Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
15 20 25

Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala
30 35 40

Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu
45 50 55 60

Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys
65 70 75

Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu
80 85 90

Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser
95 100 105

Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn
110 115 120

Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe
125 130 135 140

Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys
145 150 155

Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg
160 165 170

Gln	Leu	Pro	Ala	Ser	Gly	Lys	Val	Ile	Tyr	Lys	Gly	Val	Trp	His	Phe	
		175					180					185				
Val	Thr	Asp	Thr	Lys	Lys	Gly	Gln	Asp	Phe	Arg	Glu	Ile	Ile	Gln	Pro	
	190					195					200					
Ser	Lys	Lys	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	Gly	Ser	
205					210					215					220	
Glu	Glu	Tyr	Ser	Asn	Lys	Asn	Glu	Ser	Thr	Leu	Lys	Asp	Asp	His	Glu	
				225					230					235		
Gly	Tyr	Gly	Phe	Thr	Ser	Asn	Leu	Glu	Val	Asp	Phe	Gly	Asn	Lys	Lys	
			240						245				250			
Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Ala	Ser	Leu	Asn	Asn	Asn	Thr	
		255					260					265				
Asn	Asn	Asp	Lys	His	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	Gln	Ile	
		270				275					280					
Thr	Gly	Asn	Arg	Phe	Asn	Gly	Thr	Ala	Thr	Ala	Thr	Asp	Lys	Lys	Glu	
285					290					295					300	
Asn	Glu	Thr	Lys	Leu	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	
				305					310					315		
Gly	Gly	Phe	Phe	Gly	Pro	Gln	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	
			320					325					330			
Ser	Asp	Asp	Gln	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp	
		335					340					345				
Lys	Leu	Glu	Asn	Gly	Ala	Ala	Ala	Ser	Gly	Ser	Thr	Gly	Ala	Ala	Ala	
		350				355						360				
Ser	Gly	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys	Leu	Thr	Thr	
365					370					375					380	
Val	Leu	Asp	Ala	Val	Glu	Leu	Thr	Leu	Asn	Asp	Lys	Lys	Ile	Lys	Asn	
				385					390					395		
Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	
			400					405					410			
Ile	Pro	Leu	Leu	Pro	Lys	Asp	Ser	Glu	Ser	Gly	Asn	Thr	Gln	Ala	Asp	
		415					420					425				
Lys	Gly	Lys	Asn	Gly	Gly	Thr	Glu	Phe	Thr	Arg	Lys	Phe	Glu	His	Thr	
		430				435					440					
Pro	Glu	Ser	Asp	Lys	Lys	Asp	Ala	Gln	Ala	Gly	Thr	Gln	Thr	Asn	Gly	
445					450					455					460	

B. cont.

Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys
465 470 475

Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
480 485 490

Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly
495 500 505

Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
510 515 520

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln
525 530 535 540

Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr
545 550 555

Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
560 565 570

Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala
575 580 585

Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly
590 595 600

Bj.
Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu
605 610 615 620

Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala
625 630 635

Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
640 645 650

Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr
655 660 665

Ser Ser Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala
670 675 680

Lys Arg Gln Gln Pro Val Gln
685 690

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
(B) STRAIN: IM2394

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 1..60

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 61..1797

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..1797

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 61..1035

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1036..1386

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1387..1797

(ix) FEATURE:

- (A) NAME/KEY: misc_binding
(B) LOCATION: 46..1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT 48
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe
-20 -15 -10 -5

TTG TTG AGT GCT TGT CTG GGT GGC GGC GGC AGT TTC GAT TTG GAC AGC 96
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser
1 5 10

GTG GAA ACC GTG CAA GAT ATG CAC TCC AAA CCT AAG TAT GAG GAT GAA 144
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu
15 20 25

AAA AGC CAG CCT GAA AGC CAA CAG GAT GTA TCG GAA AAC AGC GGC GCG 192
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala
30 35 40

GCT TAT GGC TTT GCA GTA AAA CTA CCT CGC CGG AAT GCA CAT TTT AAT 240
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn
45 50 55 60

CCT	AAA	TAT	AAG	GAA	AAG	CAC	AAA	CCA	TTG	GGT	TCA	ATG	GAT	TGG	AAA	288
Pro	Lys	Tyr	Lys	Glu	Lys	His	Lys	Pro	Leu	Gly	Ser	Met	Asp	Trp	Lys	
				65					70					75		
AAA	CTG	CAA	AGA	GGA	GAA	CCA	AAT	AGT	TTT	AGT	GAG	AGG	GAT	GAA	TTG	336
Lys	Leu	Gln	Arg	Gly	Glu	Pro	Asn	Ser	Phe	Ser	Glu	Arg	Asp	Glu	Leu	
			80					85					90			
GAA	AAA	AAA	CGG	GGT	AGT	TCT	GAA	CTT	ATT	GAA	TCA	AAA	TGG	GAA	GAT	384
Glu	Lys	Lys	Arg	Gly	Ser	Ser	Glu	Leu	Ile	Glu	Ser	Lys	Trp	Glu	Asp	
		95					100					105				
GGG	CAA	AGT	CGT	GTA	GTT	GGT	TAT	ACA	AAT	TTC	ACT	TAT	GTC	CGT	TCG	432
Gly	Gln	Ser	Arg	Val	Val	Gly	Tyr	Thr	Asn	Phe	Thr	Tyr	Val	Arg	Ser	
	110					115					120					
GGA	TAT	GTT	TAC	CTT	AAT	AAA	AAT	AAT	ATT	GAT	ATT	AAG	AAT	AAT	ATA	480
Gly	Tyr	Val	Tyr	Leu	Asn	Lys	Asn	Asn	Ile	Asp	Ile	Lys	Asn	Asn	Ile	
125				130						135					140	
GTT	CTT	TTT	GGA	CCT	GAC	GGA	TAT	CTT	TAC	TAT	AAA	GGG	AAA	GAA	CCT	528
Val	Leu	Phe	Gly	Pro	Asp	Gly	Tyr	Leu	Tyr	Tyr	Lys	Gly	Lys	Glu	Pro	
			145					150						155		
TCC	AAG	GAG	CTG	CCA	TCG	GAA	AAG	ATA	ACT	TAT	AAA	GGT	ACT	TGG	GAT	576
Ser	Lys	Glu	Leu	Pro	Ser	Glu	Lys	Ile	Thr	Tyr	Lys	Gly	Thr	Trp	Asp	
			160					165					170			
TAT	GTT	ACT	GAT	GCT	ATG	GAA	AAA	CAA	AGG	TTT	GAA	GGA	TTG	GGT	AGT	624
Tyr	Val	Thr	Asp	Ala	Met	Glu	Lys	Gln	Arg	Phe	Glu	Gly	Leu	Gly	Ser	
		175					180					185				
GCA	GCA	GGA	GGA	GAT	AAA	TCG	GGG	GCG	TTG	TCT	GCA	TTA	GAA	GAA	GGG	672
Ala	Ala	Gly	Gly	Asp	Lys	Ser	Gly	Ala	Leu	Ser	Ala	Leu	Glu	Glu	Gly	
	190					195					200					
GTA	TTG	CGT	AAT	CAG	GCA	GAG	GCA	TCA	TCC	GGT	CAT	ACC	GAT	TTT	GGT	720
Val	Leu	Arg	Asn	Gln	Ala	Glu	Ala	Ser	Ser	Gly	His	Thr	Asp	Phe	Gly	
205				210						215					220	
ATG	ACT	AGT	GAG	TTT	GAG	GTT	GAT	TTT	TCT	GAT	AAA	ACA	ATA	AAG	GGC	768
Met	Thr	Ser	Glu	Phe	Glu	Val	Asp	Phe	Ser	Asp	Lys	Thr	Ile	Lys	Gly	
			225					230						235		
ACA	CTT	TAT	CGT	AAC	AAC	CGT	ATT	ACT	CAA	AAT	AAT	AGT	GAA	AAC	AAA	816
Thr	Leu	Tyr	Arg	Asn	Asn	Arg	Ile	Thr	Gln	Asn	Asn	Ser	Glu	Asn	Lys	
			240				245						250			
CAA	ATA	AAA	ACT	ACG	CGT	TAC	ACC	ATT	CAA	GCA	ACT	CTT	CAC	GGC	AAC	864
Gln	Ile	Lys	Thr	Thr	Arg	Tyr	Thr	Ile	Gln	Ala	Thr	Leu	His	Gly	Asn	
		255					260					265				

6
cont.

CGT	TTC	AAA	GGT	AAG	GCG	TTG	GCG	GCA	GAT	AAA	GGT	GCA	ACA	AAT	GGA	912
Arg	Phe	Lys	Gly	Lys	Ala	Leu	Ala	Ala	Asp	Lys	Gly	Ala	Thr	Asn	Gly	
270						275					280					
AGT	CAT	CCC	TTT	ATT	TCC	GAC	TCC	GAC	AGT	TTG	GAA	GGC	GGA	TTT	TAC	960
Ser	His	Pro	Phe	Ile	Ser	Asp	Ser	Asp	Ser	Leu	Glu	Gly	Gly	Phe	Tyr	
285					290					295					300	
GGG	CCG	AAA	GGC	GAG	GAA	CTT	GCC	GGT	AAA	TTC	TTG	AGC	AAC	GAC	AAC	1008
Gly	Pro	Lys	Gly	Glu	Glu	Leu	Ala	Gly	Lys	Phe	Leu	Ser	Asn	Asp	Asn	
				305					310					315		
AAA	GTT	GCA	GCG	GTG	TTT	GGT	GCG	AAG	CAG	AAA	GAT	AAG	AAG	GAT	GGG	1056
Lys	Val	Ala	Ala	Val	Phe	Gly	Ala	Lys	Gln	Lys	Asp	Lys	Lys	Asp	Gly	
			320					325					330			
GAA	AAC	GCG	GCA	GGG	CCT	GCA	ACG	GAA	ACC	GTG	ATA	GAT	GCA	TAC	CGT	1104
Glu	Asn	Ala	Ala	Gly	Pro	Ala	Thr	Glu	Thr	Val	Ile	Asp	Ala	Tyr	Arg	
		335					340					345				
ATT	ACC	GGC	GAG	GAG	TTT	AAG	AAA	GAG	CAA	ATA	GAC	AGT	TTT	GGA	GAT	1152
Ile	Thr	Gly	Glu	Glu	Phe	Lys	Lys	Glu	Gln	Ile	Asp	Ser	Phe	Gly	Asp	
	350					355					360					
GTG	AAA	AAG	CTG	CTG	GTT	GAC	GGA	GTG	GAG	CTT	TCA	CTG	CTG	CCG	TCT	1200
Val	Lys	Lys	Leu	Leu	Val	Asp	Gly	Val	Glu	Leu	Ser	Leu	Leu	Pro	Ser	
365					370					375					380	
GAG	GGC	AAT	AAG	GCG	GCA	TTT	CAG	CAC	GAG	ATT	GAG	CAA	AAC	GGC	GTG	1248
Glu	Gly	Asn	Lys	Ala	Ala	Phe	Gln	His	Glu	Ile	Glu	Gln	Asn	Gly	Val	
				385					390					395		
AAG	GCA	ACG	GTG	TGT	TGT	TCC	AAC	TTG	GAT	TAC	ATG	AGT	TTT	GGG	AAG	1296
Lys	Ala	Thr	Val	Cys	Cys	Ser	Asn	Leu	Asp	Tyr	Met	Ser	Phe	Gly	Lys	
			400					405					410			
CTG	TCA	AAA	GAA	AAT	AAA	GAC	GAT	ATG	TTC	CTG	CAA	GGT	GTC	CGC	ACT	1344
Leu	Ser	Lys	Glu	Asn	Lys	Asp	Asp	Met	Phe	Leu	Gln	Gly	Val	Arg	Thr	
		415					420					425				
CCA	GTA	TCC	GAT	GTG	GCG	GCA	AGG	ACG	GAG	GCA	AAC	GCC	AAA	TAT	CGC	1392
Pro	Val	Ser	Asp	Val	Ala	Ala	Arg	Thr	Glu	Ala	Asn	Ala	Lys	Tyr	Arg	
	430					435					440					
GGT	ACT	TGG	TAC	GGA	TAT	ATT	GCC	AAC	GGC	ACA	AGC	TGG	AGC	GGC	GAA	1440
Gly	Thr	Trp	Tyr	Gly	Tyr	Ile	Ala	Asn	Gly	Thr	Ser	Trp	Ser	Gly	Glu	
445					450					455					460	
GCC	TCC	AAT	CAG	GAA	GGT	GGT	AAT	AGG	GCA	GAG	TTT	GAC	GTG	GAT	TTT	1488
Ala	Ser	Asn	Gln	Glu	Gly	Gly	Asn	Arg	Ala	Glu	Phe	Asp	Val	Asp	Phe	
				465					470					475		

6 cont.

TCC ACT AAA AAA ATC AGT GGC ACA CTG ACG GCA AAA GAC CGT ACG TCT	1536
Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser	
480 485 490	
CCT GCG TTT ACT ATT ACT GCC ATG ATT AAG GAC AAC GGT TTT TCA GGT	1584
Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly	
495 500 505	
GTG GCG AAA ACC GGT GAA AAC GGC TTT GCG CTG GAT CCG CAA AAT ACC	1632
Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr	
510 515 520	
GGA AAT TCC CAC TAT ACG CAT ATT GAA GCC ACT GTA TCC GGC GGT TTC	1680
Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe	
525 530 535 540	
TAC GGC AAA AAC GCC ATC GAG ATG GGC GGA TCG TTC TCA TTT CCG GGA	1728
Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly	
545 550 555	
AAT GCA CCA GAG GGA AAA CAA GAA AAA GCA TCG GTG GTA TTC GGT GCG	1776
Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala	
560 565 570	
AAA CGC CAA CAG CTT GTG CAA TAAGCACGGC T	1808
Lys Arg Gln Gln Leu Val Gln	
575	

b cont.
(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	
-20 -15 -10 -5	
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser	
1 5 10	
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu	
15 20 25	
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala	
30 35 40	
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn	
45 50 55 60	

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys
 65 70 75
 Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu
 80 85 90
 Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp
 95 100 105
 Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser
 110 115 120
 Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile
 125 130 135 140
 Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro
 145 150 155
 Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp
 160 165 170
 Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser
 175 180 185
 Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly
 190 195 200
 Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly
 205 210 215 220
 Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly
 225 230 235
 Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys
 240 245 250
 Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn
 255 260 265
 Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly
 270 275 280
 Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr
 285 290 295 300
 Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn
 305 310 315
 Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly
 320 325 330
 Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg
 335 340 345

Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp
 350 355 360
 Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser
 365 370 375 380
 Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val
 385 390 395
 Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys
 400 405 410
 Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr
 415 420 425
 Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg
 430 435 440
 Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu
 445 450 455 460
 Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe
 465 470 475
 Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser
 480 485 490
 Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly
 495 500 505
 Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr
 510 515 520
 Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe
 525 530 535 540
 Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly
 545 550 555
 Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala
 560 565 570
 Lys Arg Gln Gln Leu Val Gln
 575

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: N. meningitidis
(B) STRAIN: M978

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..2115

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGT	CTG	GGT	GGC	GGC	GGC	ACG	TTC	GAT	CTT	GAT	TCT	GTC	GAT	ACC	GAA	48
Cys	Leu	Gly	Gly	Gly	Gly	Thr	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	Glu	
1				5					10					15		
GCC	CCG	CGT	CCC	GCC	CCA	AAA	TAT	CAA	GAT	GTT	TCT	TCC	GAA	AAA	CCG	96
Ala	Pro	Arg	Pro	Ala	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	Pro	
			20					25					30			
CAA	GCC	CAA	AAA	GAC	CAA	GGC	GGA	TAC	GGT	TTT	GCA	ATG	CGC	CTC	AAG	144
Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	Lys	
		35				40					45					
CGG	CGG	AAT	TGG	CAT	CCG	CAG	GCA	AAT	CCT	AAA	GAA	GAT	GAG	ATA	AAA	192
Arg	Arg	Asn	Trp	His	Pro	Gln	Ala	Asn	Pro	Lys	Glu	Asp	Glu	Ile	Lys	
B. y. cont.	50					55					60					
CTT	TCT	GAA	AAT	GAT	TGG	GAG	GCG	ACA	GGA	TTG	CCA	GGC	AAT	CCC	AAA	240
Leu	Ser	Glu	Asn	Asp	Trp	Glu	Ala	Thr	Gly	Leu	Pro	Gly	Asn	Pro	Lys	
65					70				75						80	
AAC	TTA	CCT	GAG	CGA	CAG	AAA	TCG	GTT	ATT	GAA	AAA	GTA	AAA	ACA	GGC	288
Asn	Leu	Pro	Glu	Arg	Gln	Lys	Ser	Val	Ile	Glu	Lys	Val	Lys	Thr	Gly	
				85					90					95		
AGC	GAC	AGC	AAT	ATT	TAT	TCT	TCC	CCC	TAT	CTC	ACG	CAA	TCA	AAC	CAT	336
Ser	Asp	Ser	Asn	Ile	Tyr	Ser	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	Asn	His	
			100					105					110			
CAA	AAC	GGC	AGT	GCA	AAC	CAA	CCA	AAA	AAT	GAA	GTA	AAA	GAT	TAT	AAA	384
Gln	Asn	Gly	Ser	Ala	Asn	Gln	Pro	Lys	Asn	Glu	Val	Lys	Asp	Tyr	Lys	
		115					120					125				
GAG	TTC	AAA	TAT	GTT	TAT	TCC	GGT	TGG	TTT	TAC	AAA	CAC	GCT	AAA	CTC	432
Glu	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	Tyr	Lys	His	Ala	Lys	Leu	
	130					135					140					
GAA	ATC	ATA	AAA	GAA	AAC	AAC	TTA	ATT	AAG	GGT	GCA	AAG	AGC	GGC	GAC	480
Glu	Ile	Ile	Lys	Glu	Asn	Asn	Leu	Ile	Lys	Gly	Ala	Lys	Ser	Gly	Asp	
145					150					155					160	

GAC Asp	GGT Gly	TAT Tyr	ATC Ile	TTT Phe 165	TAT Tyr	CAC His	GGT Gly	GAA Glu 170	AAA Lys	CCT Pro	TCC Ser	CGA Arg	CAA Gln	CTT Leu 175	CCC Pro	528
GTT Val	TCT Ser	GGA Gly	GAA Glu 180	GTT Val	ACC Thr	TAC Tyr	AAA Lys	GGC Gly 185	GTA Val	TGG Trp	CAT His	TTT Phe	GTA Val 190	ACC Thr	GAT Asp	576
ACG Thr	AAA Lys	CAG Gln 195	GGA Gly	CAA Gln	AAA Lys	TTT Phe	AAC Asn 200	GAT Asp	ATT Ile	CTT Leu	GGA Gly	ACC Thr 205	TCA Ser	AAA Lys	AAA Lys	624
CAA Gln 210	GGC Gly	GAC Asp	AGG Arg	TAT Tyr	AGC Ser	GGA Gly 215	TTT Phe	CCG Pro	GGT Gly	GAT Asp	GAC Asp 220	GGC Gly	GAA Glu	GAA Glu	TAT Tyr	672
TCC Ser 225	AAT Asn	AAA Lys	AAT Asn	GAA Glu 230	GCG Ala	ACT Thr	TTA Leu	CAA Gln	GGC Gly	AGT Ser 235	CAA Gln	GAG Glu	GGT Gly	TAT Tyr	GGT Gly 240	720
TTT Phe	ACC Thr	TCA Ser	AAT Asn 245	TTA Leu	AAA Lys	GTG Val	GAT Asp	TTC Phe	AAT Asn 250	AAG Lys	AAA Lys	AAA Lys	TTG Leu 255	ACG Thr	GGT Gly	768
GAA (Glu cont.)	TTG Leu	ATA Ile	CGC Arg 260	AAT Asn	AAT Asn	AGA Arg	GTT Val	ACA Thr 265	AAC Asn	GCT Ala	ACT Thr	GCT Ala	AAC Asn 270	GAT Asp	AAA Lys	816
TAC Tyr	ACC Thr	ACC Thr 275	CAA Gln	TAT Tyr	TAC Tyr	AGC Ser	CTT Leu 280	GAG Glu	GCT Ala	CAA Gln	GTA Val	ACA Thr 285	GGC Gly	AAC Asn	CGC Arg	864
TTC Phe 290	AAC Asn	GGC Gly	AAG Lys	GCA Ala	ACG Thr	GCA Ala 295	ACC Thr	GAC Asp	AAA Lys	CCT Pro	GGC Gly 300	ACT Thr	GGA Gly	GAA Glu	ACC Thr	912
AAA Lys 305	CAA Gln	CAT His	CCC Pro	TTT Phe 310	GTT Val	TCC Ser	GAC Asp	TCG Ser	TCT Ser	TCT Ser 315	TTG Leu	AGC Ser	GGC Gly	GGC Gly	TTT Phe 320	960
TTC Phe	GGC Gly	CCG Pro	AAG Lys	GGT Gly 325	GAG Glu	GAA Glu	TTG Leu	GGT Gly	TTC Phe 330	CGC Arg	TTT Phe	TTG Leu	AGC Ser	AAC Asn 335	GAT Asp	1008
CAA Gln	AAA Lys	GTT Val 340	GCC Ala	GTT Val	GTC Val	GGC Gly	AGC Ser	GCG Ala 345	AAA Lys	ACC Thr	CAA Gln	GAC Asp	AAA Lys 350	GCC Ala	GCA Ala	1056
AAT Asn	GGC Gly	AAT Asn 355	ACT Thr	GCG Ala	GCG Ala	GCT Ala	TCA Ser 360	GGC Gly	GGC Gly	ACA Thr	GAT Asp	GCG Ala 365	GCA Ala	GCA Ala	TCA Ser	1104

AAC Asn 370	GGT Gly	GCG Ala	GCA Ala	GGC Gly	ACG Thr	TCG Ser	TCT Ser	GAA Glu	AAC Asn	AGT Ser	AAG Lys	CTG Leu	ACC Thr	ACG Thr	GTT Val	1152
TTG Leu 385	GAT Asp	GCG Ala	GTT Val	GAA Glu	TTG Leu	ACA Thr	CTA Leu	AAC Asn	GAC Asp	AAG Lys	AAA Lys	ATC Ile	AAA Lys	AAT Asn	CTC Leu	1200
GAC Asp	AAC Asn	TTC Phe	AGC Ser	AAT Asn 405	GCC Ala	GCC Ala	CAA Gln	CTG Leu	GTT Val 410	GTC Val	GAC Asp	GGC Gly	ATT Ile	ATG Met 415	ATT Ile	1248
CCG Pro	CTC Leu	CTG Leu	CCC Pro	GAG Glu 420	ACT Thr	TCC Ser	GAA Glu	AGT Ser	GGG Gly	AGC Ser	AAT Asn	CAG Gln	GCA Ala 430	GAT Asp	AAA Lys	1296
GGT Gly	AAA Lys 435	AAA Lys	GGT Gly	AAA Lys	AAC Asn	GGT Gly	AAA Lys 440	AAC Asn	GGC Gly	GGA Gly	ACA Thr	GAC Asp 445	TTT Phe	ACC Thr	TAC Tyr	1344
AAA Lys 450	ACA Thr	ACC Thr	TAC Tyr	ACG Thr	CCG Pro	AAA Lys 455	AAC Asn	GAT Asp	GAC Asp	AAA Lys	GAT Asp 460	ACC Thr	AAA Lys	GCC Ala	CAA Gln	1392
ACA Thr 465	GGT Gly	GCG Ala	GCA Ala	GGC Gly	TCT Ser	AGC Ser	GGC Gly	GCA Ala	CAA Gln	ACC Thr 475	GAT Asp	TTG Leu	GGT Gly	AAG Lys	GCG Ala 480	1440
GAC Asp	GTT Val	AAC Asn	GGC Gly	GGT Gly 485	AAG Lys	GCA Ala	GAA Glu	ACA Thr	AAA Lys 490	ACC Thr	TAT Tyr	GAA Glu	GTC Val	GAA Glu 495	GTC Val	1488
TGC Cys	TGT Cys	TCC Ser	AAC Asn	CTC Leu	AAT Asn	TAT Tyr	CTG Leu	AAA Lys 505	TAC Tyr	GGA Gly	ATG Met	TTG Leu	ACG Thr	CGT Arg	AAA Lys	1536
AAC Asn	AGC Ser	AAG Lys	TCC Ser	GCG Ala	ATG Met	CAG Gln	GCA Ala	GGA Gly	GGA Gly	AAC Asn	AGT Ser	AGT Ser	CAA Gln	GCT Ala	GAT Asp	1584
GCT Ala 530	AAA Lys	ACG Thr	GAA Glu	CAA Gln	GTT Val	GAA Glu 535	CAA Gln	AGT Ser	ATG Met	TTC Phe	CTC Leu	CAA Gln	GGC Gly	GAG Glu	CGT Arg	1632
ACC Thr 545	GAT Asp	GAA Glu	AAA Lys	GAG Glu	ATT Ile 550	CCA Pro	AAC Asn	GAC Asp	CAA Gln	AAC Asn 555	GTC Val	GTT Val	TAT Tyr	CGG Arg	GGG Gly 560	1680
TCT Ser	TGG Trp	TAC Tyr	GGG Gly	CAT His 565	ATT Ile	GCC Ala	AGC Ser	AGC Ser	ACA Thr 570	AGC Ser	TGG Trp	AGC Ser	GGC Gly	AAT Asn 575	GCT Ala	1728

TCC AAT GCA ACG AGT GGC AAC AGG GCG GAA TTT ACT GTG AAT TTC GAT	1776
Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp	
580 585 590	
ACG AAA AAA ATT AAC GGC ACG TTA ACC GCT GAA AAC AGG CAG GAG GCA	1824
Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala	
595 600 605	
ACC TTT ACC ATT GAT GGT AAG ATT GAG GGC AAC GGT TTT TCC GGT ACC	1872
Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr	
610 615 620	
GCA AAA ACT GCT GAC TTA GGT TTT GAT CTC GAT CAA AGC AAT ACC ACC	1920
Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr	
625 630 635 640	
GGC ACG CCT AAG GCA TAT ATC ACA GAT GCC AAG GTG CAG GGC GGT TTT	1968
Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe	
645 650 655	
TAC GGG CCT AAA GCC GAA GAG TTG GGC GGA TGG TTT GCC TAT CCG GGC	2016
Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly	
660 665 670	
GAT AAA CAA ACG GAA AAG GCA ACG GTT GCA TCC GGC GAT GGA AAT TCA	2064
Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser	
675 680 685	
GCA AGC AGC GCG ACC GTG GTA TTC GGT GCG AAA CGC CAA CAG CCT GTG	2112
Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val	
690 695 700	
CAA TAACTAAATG AAGTTGTCTG GGTGGCGGCG GCACGTTCGA TCTTGATTCT	2165
Gln	
705	
GTCGATACCG AAGCCCCGCG TCCCGCCCCA AAATATCAAG ATGTTTCTTC CGAAAAACCG	2225
CAAGCCCAAA AAGACCAAGG CGGATACGGT	2255

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Leu	Gly	Gly	Gly	Gly	Thr	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	Glu
1				5					10					15	

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro
20 25 30

Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys
35 40 45

Arg Arg Asn Trp His Pro Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys
50 55 60

Leu Ser Glu Asn Asp Trp Glu Ala Thr Gly Leu Pro Gly Asn Pro Lys
65 70 75 80

Asn Leu Pro Glu Arg Gln Lys Ser Val Ile Glu Lys Val Lys Thr Gly
85 90 95

Ser Asp Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser Asn His
100 105 110

Gln Asn Gly Ser Ala Asn Gln Pro Lys Asn Glu Val Lys Asp Tyr Lys
115 120 125

Glu Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala Lys Leu
130 135 140

Glu Ile Ile Lys Glu Asn Asn Leu Ile Lys Gly Ala Lys Ser Gly Asp
145 150 155 160

Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg Gln Leu Pro
165 170 175

Val Ser Gly Glu Val Thr Tyr Lys Gly Val Trp His Phe Val Thr Asp
180 185 190

Thr Lys Gln Gly Gln Lys Phe Asn Asp Ile Leu Gly Thr Ser Lys Lys
195 200 205

Gln Gly Asp Arg Tyr Ser Gly Phe Pro Gly Asp Asp Gly Glu Glu Tyr
210 215 220

Ser Asn Lys Asn Glu Ala Thr Leu Gln Gly Ser Gln Glu Gly Tyr Gly
225 230 235 240

Phe Thr Ser Asn Leu Lys Val Asp Phe Asn Lys Lys Lys Leu Thr Gly
245 250 255

Glu Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Thr Ala Asn Asp Lys
260 265 270

Tyr Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly Asn Arg
275 280 285

Phe Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Gly Thr Gly Glu Thr
290 295 300

8.
ent.

Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe
 305 310 315 320
 Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asn Asp
 325 330 335
 Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Gln Asp Lys Ala Ala
 340 345 350
 Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly Thr Asp Ala Ala Ala Ser
 355 360 365
 Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val
 370 375 380
 Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu
 385 390 395 400
 Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile
 405 410 415
 Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Ser Asn Gln Ala Asp Lys
 420 425 430
 Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr
 435 440 445
 Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln
 450 455 460
 Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln Thr Asp Leu Gly Lys Ala
 465 470 475 480
 Asp Val Asn Gly Gly Lys Ala Glu Thr Lys Thr Tyr Glu Val Glu Val
 485 490 495
 Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys
 500 505 510
 Asn Ser Lys Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp
 515 520 525
 Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg
 530 535 540
 Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly
 545 550 555 560
 Ser Trp Tyr Gly His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala
 565 570 575
 Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp
 580 585 590

Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala
 595 600 605
 Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr
 610 615 620
 Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr
 625 630 635 640
 Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe
 645 650 655
 Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
 660 665 670
 Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser
 675 680 685
 Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val
 690 695 700
 Gln
 705

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
 (B) STRAIN: 6940

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..2079

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..2079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGT TTG GGT GGC GGC GGC ACG TTC GAT CTT GAT TCT GTC GAT ACC GAA
 Cys Leu Gly Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu
 1 5 10 15

GCC	CCG	CGT	CCC	GAC	CCA	AAG	TAT	CAA	GAT	GTT	TCT	TCC	GAA	AAA	CCG	96
Ala	Pro	Arg	Pro	Asp	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	Pro	
			20					25					30			
CAA	GCC	CAA	AAA	GAC	CAA	GGC	GGA	TAC	GGT	TTT	GCG	ATG	AGG	TTG	AAA	144
Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	Lys	
		35				40					45					
CGG	AGG	AAT	TGG	TAT	TCC	GCA	GCA	AAA	GAA	GAC	GAG	GTT	AAA	CTG	AAC	192
Arg.	Arg	Asn	Trp	Tyr	Ser	Ala	Ala	Lys	Glu	Asp	Glu	Val	Lys	Leu	Asn	
	50					55					60					
GAG	AGT	GAT	TGG	GAG	ACG	ACA	GGA	TTG	CCG	ACA	GAA	CCC	AAG	AAA	CTG	240
Glu	Ser	Asp	Trp	Glu	Thr	Thr	Gly	Leu	Pro	Thr	Glu	Pro	Lys	Lys	Leu	
65					70					75					80	
CCA	TTA	AAA	CAA	GAA	TCC	GTC	ATT	TCA	AAA	GTA	CAA	GCA	AAC	AAT	GGC	288
Pro	Leu	Lys	Gln	Glu	Ser	Val	Ile	Ser	Lys	Val	Gln	Ala	Asn	Asn	Gly	
				85					90					95		
GAC	AAC	AAT	ATT	TAC	ACT	TCC	CCC	TAT	CTC	ACG	CAA	TCA	AAC	CAT	CAA	336
Asp	Asn	Asn	Ile	Tyr	Thr	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	Asn	His	Gln	
			100					105					110			
AAT	AGC	AGC	ATT	AAT	GGC	GGT	GCA	AAC	CTG	CCA	AAA	AAC	GAA	GTA	ACA	384
Asn	Ser	Ser	Ile	Asn	Gly	Gly	Ala	Asn	Leu	Pro	Lys	Asn	Glu	Val	Thr	
		115				120						125				
AAT	TAT	AAA	GAT	TTC	AAA	TAT	GTT	TAT	TCC	GGC	TGG	TTT	TAT	AAA	CAT	432
Asn	Tyr	Lys	Asp	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	Tyr	Lys	His	
	130					135					140					
GCT	AAA	AAC	GAA	ATC	ATA	AGA	GAA	AAC	AGC	TCA	ATT	AAG	GGT	GCA	AAG	480
Ala	Lys	Asn	Glu	Ile	Ile	Arg	Glu	Asn	Ser	Ser	Ile	Lys	Gly	Ala	Lys	
145					150					155					160	
AAC	GGC	GAC	GAC	GGC	TAT	ATC	TTT	TAT	CAC	GGC	AAA	GAA	CCT	TCC	CGA	528
Asn	Gly	Asp	Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Lys	Glu	Pro	Ser	Arg	
				165					170					175		
CAA	CTT	CCC	GCT	TCT	GGA	ACA	GTT	ACC	TAT	AAA	GGT	GTG	TGG	CAT	TTT	576
Gln	Leu	Pro	Ala	Ser	Gly	Thr	Val	Thr	Tyr	Lys	Gly	Val	Trp	His	Phe	
			180					185					190			
GCG	ACC	GAT	GTC	AAA	AAA	TCC	CAA	AAT	TTT	CGC	GAT	ATT	ATC	CAG	CCT	624
Ala	Thr	Asp	Val	Lys	Lys	Ser	Gln	Asn	Phe	Arg	Asp	Ile	Ile	Gln	Pro	
		195				200						205				
TCG	AAA	AAA	CAA	GGC	GAC	AGG	TAT	AGC	GGA	TTT	TCG	GGC	GAT	GAT	GAT	672
Ser	Lys	Lys	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	Asp	Asp	
	210					215					220					

GAA Glu 225	CAA Gln	TAT Tyr	TCT Ser	AAT Asn	AAA Lys 230	AAC Asn	GAA Glu	TCC Ser	ATG Met	CTG Leu 235	AAA Lys	GAT Asp	GGT Gly	CAA Gln	GAG Glu 240	720
GGT Gly	TAT Tyr	GGT Gly	TTT Phe 245	ACC Thr	TCG Ser	AAT Asn	TTA Leu	GAA Glu	GTG Val 250	GAT Asp	TTC Phe	GGC Gly	AGT Ser	AAA Lys 255	AAA Lys	768
TTG Leu	ACG Thr	GGT Gly	AAA Lys 260	TTA Leu	ATA Ile	CGC Arg	AAT Asn	AAT Asn 265	AGA Arg	GTT Val	ACA Thr	AAC Asn	GCT Ala 270	CCT Pro	ACT Thr	816
AAC Asn	GAT Asp	AAA Lys 275	TAC Tyr	ACC Thr	ACC Thr	CAA Gln	TAC Tyr 280	TAC Tyr	AGC Ser	CTT Leu	GAT Asp	GCC Ala 285	CAA Gln	ATA Ile	ACA Thr	864
GGC Gly 290	AAC Asn	CGC Arg	TTC Phe	AAC Asn	GGT Gly	AAG Lys 295	GCG Ala	ATA Ile	CGG Arg	ACC Thr	GAC Asp 300	AAA Lys	CCC Pro	GAC Asp	ACT Thr	912
GGA Gly 305	GGA Gly	ACC Thr	AAA Lys	CTA Leu	CAT His 310	CCC Pro	TTT Phe	GTT Val	TCC Ser	GAC Asp 315	TCG Ser	TCT Ser	TCT Ser	TTG Leu	AGC Ser 320	960
GGC Gly	GGC Gly	TTT Phe	TTC Phe	GGT Gly 325	CCG Pro	AAG Lys	GGT Gly	GAG Glu	GAA Glu 330	TTG Leu	GGT Gly	TTC Phe	CGC Arg	TTT Phe 335	TTG Leu	1008
AGC Ser	GAC Asp	GAT Asp	AAA Lys 340	AAA Lys	GTT Val	GCG Ala	GTT Val	GTC Val 345	GGC Gly	AGC Ser	GCG Ala	AAA Lys	ACC Thr 350	AAA Lys	GAC Asp	1056
AAA Lys	ACG Thr 355	GAA Glu	AAT Asn	GGC Gly	GCG Ala	GTG Val	GCT Ala 360	TCA Ser	GGC Gly	GGC Gly	ACA Thr	GAT Asp 365	GCG Ala	GCA Ala	GCA Ala	1104
TCA Ser 370	AAC Asn	GGT Gly	GCG Ala	GCA Ala	GGC Gly	ACG Thr 375	TCG Ser	TCT Ser	GAA Glu	AAC Asn	AGT Ser 380	AAG Lys	CTG Leu	ACC Thr	ACG Thr	1152
GTT Val 385	TTG Leu	GAT Asp	GCG Ala	GTC Val	GAG Glu 390	CTG Leu	AAA Lys	TTG Leu	GGC Gly	GAT Asp 395	AAG Lys	GAA Glu	GTC Val	CAA Gln	AAG Lys 400	1200
CTC Leu	GAC Asp	AAC Asn	TTC Phe	AGC Ser 405	AAC Asn	GCC Ala	GCC Ala	CAA Gln	CTG Leu 410	GTT Val	GTC Val	GAC Asp	GGC Gly	ATT Ile 415	ATG Met	1248
ATT Ile	CCG Pro	CTC Leu	TTG Leu 420	CCC Pro	GAG Glu	GCT Ala	TCC Ser	GAA Glu 425	AGT Ser	GGG Gly	AAC Asn	AAT Asn	CAA Gln 430	GCC Ala	AAT Asn	1296

B' *ent*

CAA GGT ACA AAT GGC GGA ACA GCC TTT ACC CGC AAA TTT GAC CAC ACG Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr 435 440 445	1344
CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly 450 455 460	1392
GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys 465 470 475 480	1440
ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr 485 490 495	1488
GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GAA Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu 500 505 510	1536
AGC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met 515 520 525	1584
TTC CTC CAA GGC GAG CGC ACC GAT GAA AAA GAG ATT CCA AGC GAG CAA Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln 530 535 540	1632
AAC ATC GTT TAT CGG GGG TCT TGG TAC GGA TAT ATT GCC AAC GAC AAA Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Lys 545 550 555 560	1680
AGC ACA AGC TGG AGC GGC AAT GCT TCC AAT GCA ACG AGT GGC AAC AGG Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg 565 570 575	1728
GCG GAA TTT ACT GTG AAT TTT GCC GAT AAA AAA ATT ACT GGT ACG TTA Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Thr Leu 580 585 590	1776
ACC GCT GAC AAC AGG CAG GAG GCA ACC TTT ACC ATT GAT GGT AAT ATT Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Asn Ile 595 600 605	1824
AAG GAC AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe 610 615 620	1872
GAT CTC GAT CAA AGC AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr 625 630 635 640	1920

GAT GCC AAG GTG CAG GGC GGT TTT TAC GGG CCC AAA GCC GAA GAG TTG	1968
Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu	
645 650 655	
GGC GGA TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG AAA AAT GCA ACA	2016
Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr	
660 665 670	
AAT GCA TCC GGC AAT AGC AGT GCA ACT GTC GTA TTC GGT GCG AAA CGC	2064
Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg	
675 680 685	
CAA CAG CCT GTG CGA TAACGCAAGC CCAAAAAGAC CAAGGCGGAT ACGGT	2114
Gln Gln Pro Val Arg	
690	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys	Leu	Gly	Gly	Gly	Gly	Thr	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	Glu
1				5					10					15	
Ala	Pro	Arg	Pro	Asp	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	Pro
			20					25					30		
Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	Lys
		35				40						45			
Arg	Arg	Asn	Trp	Tyr	Ser	Ala	Ala	Lys	Glu	Asp	Glu	Val	Lys	Leu	Asn
	50					55					60				
Glu	Ser	Asp	Trp	Glu	Thr	Thr	Gly	Leu	Pro	Thr	Glu	Pro	Lys	Lys	Leu
65				70					75					80	
Pro	Leu	Lys	Gln	Glu	Ser	Val	Ile	Ser	Lys	Val	Gln	Ala	Asn	Asn	Gly
			85						90					95	
Asp	Asn	Asn	Ile	Tyr	Thr	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	Asn	His	Gln
		100						105					110		
Asn	Ser	Ser	Ile	Asn	Gly	Gly	Ala	Asn	Leu	Pro	Lys	Asn	Glu	Val	Thr
		115					120					125			
Asn	Tyr	Lys	Asp	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	Tyr	Lys	His
	130					135					140				

Ala	Lys	Asn	Glu	Ile	Ile	Arg	Glu	Asn	Ser	Ser	Ile	Lys	Gly	Ala	Lys	145	150	155	160
Asn	Gly	Asp	Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Lys	Glu	Pro	Ser	Arg	165	170	175	
Gln	Leu	Pro	Ala	Ser	Gly	Thr	Val	Thr	Tyr	Lys	Gly	Val	Trp	His	Phe	180	185	190	
Ala	Thr	Asp	Val	Lys	Lys	Ser	Gln	Asn	Phe	Arg	Asp	Ile	Ile	Gln	Pro	195	200	205	
Ser	Lys	Lys	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	Asp	Asp	210	215	220	
Glu	Gln	Tyr	Ser	Asn	Lys	Asn	Glu	Ser	Met	Leu	Lys	Asp	Gly	Gln	Glu	225	230	235	240
Gly	Tyr	Gly	Phe	Thr	Ser	Asn	Leu	Glu	Val	Asp	Phe	Gly	Ser	Lys	Lys	245	250	255	
Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Arg	Val	Thr	Asn	Ala	Pro	Thr	260	265	270	
Asn	Asp	Lys	Tyr	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	Gln	Ile	Thr	275	280	285	
Gly	Asn	Arg	Phe	Asn	Gly	Lys	Ala	Ile	Arg	Thr	Asp	Lys	Pro	Asp	Thr	290	295	300	
Gly	Gly	Thr	Lys	Leu	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	305	310	315	320
Gly	Gly	Phe	Phe	Gly	Pro	Lys	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	325	330	335	
Ser	Asp	Asp	Lys	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp	340	345	350	
Lys	Thr	Glu	Asn	Gly	Ala	Val	Ala	Ser	Gly	Gly	Thr	Asp	Ala	Ala	Ala	355	360	365	
Ser	Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys	Leu	Thr	Thr	370	375	380	
Val	Leu	Asp	Ala	Val	Glu	Leu	Lys	Leu	Gly	Asp	Lys	Glu	Val	Gln	Lys	385	390	395	400
Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	405	410	415	
Ile	Pro	Leu	Leu	Pro	Glu	Ala	Ser	Glu	Ser	Gly	Asn	Asn	Gln	Ala	Asn	420	425	430	

Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr
435 440 445

Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly
450 455 460

Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys
465 470 475 480

Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
485 490 495

Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu
500 505 510

Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
515 520 525

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln
530 535 540

Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Lys
545 550 555 560

Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg
565 570 575

Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Thr Leu
580 585 590

Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Asn Ile
595 600 605

Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe
610 615 620

Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr
625 630 635 640

Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu
645 650 655

Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr
660 665 670

Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg
675 680 685

Gln Gln Pro Val Arg
690

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: S3032

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..2097

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGT	TTG	GGC	GGA	GGC	GGC	GGC	AGT	TTC	GAT	CTT	GAT	TCT	GTC	GAT	ACC	48
Cys	Leu	Gly	Gly	Gly	Gly	Gly	Ser	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	
1				5					10					15		
GAA	GCC	CCG	CGT	CCC	GCG	CCA	AAG	TAT	CAA	GAT	GTT	TCT	TCC	GAA	AAA	96
Glu	Ala	Pro	Arg	Pro	Ala	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	
			20					25					30			
CCG	CAA	GCC	CAA	AAA	GAC	CAA	GGC	GGA	TAC	GGT	TTT	GCG	ATG	AGG	TTG	144
Pro	Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	
		35					40					45				
AAA	CGG	AGG	AAT	TGG	TAT	CCG	TCG	GCA	AAA	GAA	AAC	GAG	GTT	AAA	CTG	192
Lys	Arg	Arg	Asn	Trp	Tyr	Pro	Ser	Ala	Lys	Glu	Asn	Glu	Val	Lys	Leu	
	50					55					60					
AAT	GAG	AGT	GAT	TGG	GAG	ACG	ACA	GGA	TTG	CCA	AGC	AAT	CCC	AAA	AAC	240
Asn	Glu	Ser	Asp	Trp	Gln	Thr	Thr	Gly	Leu	Pro	Ser	Asn	Pro	Lys	Asn	
	65				70					75					80	
TTA	CCT	GAG	CGA	CAG	AAA	TCG	GTT	ATT	GAT	CAA	GTA	GAA	ACA	GAT	GGC	288
Leu	Pro	Glu	Arg	Gln	Lys	Ser	Val	Ile	Asp	Gln	Val	Glu	Thr	Asp	Gly	
			85						90					95		
GAC	AGC	AAT	AAC	AGC	AAT	ATT	TAT	TCT	TCC	CCC	TAT	CTC	ACG	CAA	TCA	336
Asp	Ser	Asn	Asn	Ser	Asn	Ile	Tyr	Ser	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	
		100						105						110		

AAC Asn	CAT His	CAA Gln 115	AAC Asn	GGC Gly	AAC Asn	ACT Thr	GGC Gly 120	AAC Asn	GGT Gly	GTA Val	AAC Asn	CAA Gln 125	CCA Pro	AAA Lys	AAC Asn	384
GAA Glu 130	GTA Val	ACA Thr	GAT Asp	TAC Tyr	AAA Lys	AAT Asn 135	TTT Phe	AAA Lys	TAT Tyr	GTT Val	TAT Tyr 140	TCC Ser	GGC Gly	TGG Trp	TTT Phe	432
TAC Tyr 145	AAA Lys	CAC His	GCC Ala	AAA Lys	CGA Arg 150	GAG Glu	GTT Val	AAC Asn	TTA Leu	GCG Ala 155	GTG Val	GAA Glu	CCT Pro	AAA Lys	ATT Ile 160	480
GCA Ala	AAA Lys	AAC Asn	GGC Gly	GAC Asp 165	GAC Asp	GGT Gly	TAT Tyr	ATC Ile	TTC Phe 170	TAT Tyr	CAC His	GGT Gly	AAA Lys	GAC Asp 175	CCT Pro	528
TCC Ser	CGA Arg	CAA Gln	CTT Leu 180	CCC Pro	GCT Ala	TCT Ser	GGA Gly 185	AAA Lys	ATT Ile	ACC Thr	TAT Tyr	AAA Lys 190	GGT Gly	GTG Val	TGG Trp	576
CAT His	TTT Phe 195	GCG Ala	ACC Thr	GAT Asp	ACA Thr	AAA Lys 200	AGG Arg	GGT Gly	CAA Gln	AAA Lys	TTT Phe 205	CGT Arg	GAA Glu	ATT Ile	ATC Ile	624
CAA Gln 210	CCT Pro	TCA Ser	AAA Lys	AAT Asn	CAA Gln	GGC Gly 215	GAC Asp	AGA Arg	TAT Tyr	AGC Ser	GGA Gly 220	TTT Phe	TCG Ser	GGT Gly	GAT Asp	672
GAT Asp 225	GAT Asp	GAA Glu	CAA Gln	TAT Tyr	TCT Ser 230	AAT Asn	AAA Lys	AAC Asn	GAA Glu 235	TCC Ser	ATG Met	CTG Leu	AAA Lys	GAT Asp	GGT Gly 240	720
CAT His	GAA Glu	GGT Gly	TAT Tyr 245	GGT Gly	TTT Phe	GCC Ala	TCG Ser	AAT Asn 250	TTA Leu	GAA Glu	GTG Val	GAT Asp	TTC Phe	GAC Asp 255	AAT Asn	768
AAA Lys	AAA Lys	TTG Leu	ACG Thr 260	GGT Gly	AAA Lys	TTA Leu	ATA Ile 265	CGC Arg	AAT Asn	AAT Asn	GCG Ala	AAC Asn	CAA Gln 270	AAT Asn	AAT Asn	816
AAT Asn	ACT Thr	AAT Asn 275	AAT Asn	GAC Asp	AAA Lys	CAC His	ACC Thr 280	ACC Thr	CAA Gln	TAC Tyr	TAC Tyr	AGC Ser 285	CTT Leu	GAT Asp	GCG Ala	864
ACG Thr 290	CTT Leu	AAG Lys	GGA Gly	AAC Asn	CGC Arg	TTC Phe 295	AGC Ser	GGA Gly	AAA Lys	GCG Ala	GAA Glu 300	GCA Ala	ACC Thr	GAC Asp	AAA Lys	912
CCC Pro 305	AAA Lys	AAC Asn	GAC Asp	GGC Gly	GAA Glu 310	ACC Thr	AAG Lys	GAA Glu	CAT His	CCC Pro 315	TTT Phe	GTT Val	TCC Ser	GAC Asp	TCG Ser 320	960

6 cont

TCT	TCT	TTG	AGC	GGC	GGC	TTT	TTC	GGC	CCG	CAG	GGT	GAG	GAA	TTG	GGT	1008
Ser	Ser	Leu	Ser	Gly	Gly	Phe	Phe	Gly	Pro	Gln	Gly	Glu	Glu	Leu	Gly	
				325					330					335		
TTC	CGC	TTT	TTG	AGC	AAC	GAT	CAA	AAA	GTT	GCC	GTT	GTC	GGC	AGC	GCG	1056
Phe	Arg	Phe	Leu	Ser	Asn	Asp	Gln	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	
			340					345					350			
AAA	ACC	AAA	GAC	AAA	CCC	GCA	AAT	GGC	AAT	ACT	GCG	GAG	GCT	TCA	GGC	1104
Lys	Thr	Lys	Asp	Lys	Pro	Ala	Asn	Gly	Asn	Thr	Ala	Glu	Ala	Ser	Gly	
		355					360					365				
GGC	ACA	GAT	GCG	GCA	GCA	TCG	GGC	GGT	GCG	GCA	GGC	ACG	TCG	TCT	GAA	1152
Gly	Thr	Asp	Ala	Ala	Ala	Ser	Gly	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	
	370					375					380					
AAC	AGT	AAG	CTG	ACC	ACG	GTT	TTG	GAT	GCG	GTC	GAG	CTG	ACG	CAC	GGC	1200
Asn	Ser	Lys	Leu	Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	Thr	His	Gly	
385					390					395					400	
GGC	ACA	GCA	ATC	AAA	AAT	CTC	GAC	AAC	TTC	AGC	AAT	GCC	GCC	CAA	CTG	1248
Gly	Thr	Ala	Ile	Lys	Asn	Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	
			405						410					415		
GTT	GTC	GAC	GGC	ATT	ATG	ATT	CCG	CTC	CTG	CCT	CAA	AAT	TCA	ACA	GGC	1296
Val	Val	Asp	Gly	Ile	Met	Ile	Pro	Leu	Leu	Pro	Gln	Asn	Ser	Thr	Gly	
			420					425					430			
AAA	AAT	AAT	CAG	CCC	GAT	CAA	GGT	AAA	AAC	GGC	GGA	ACA	GCC	TTT	ATC	1344
Lys	Asn	Asn	Gln	Pro	Asp	Gln	Gly	Lys	Asn	Gly	Gly	Thr	Ala	Phe	Ile	
		435					440					445				
TAT	AAA	ACG	ACC	TAC	ACG	CCG	AAA	AAC	GAT	GAC	AAA	GAT	ACC	AAA	GCC	1392
Tyr	Lys	Thr	Thr	Tyr	Thr	Pro	Lys	Asn	Asp	Asp	Lys	Asp	Thr	Lys	Ala	
	450					455					460					
CAA	ACA	GTC	ACG	GGC	GGC	ACG	CAA	ACC	GCT	TCA	AAT	ACG	GCA	GGT	GAT	1440
Gln	Thr	Val	Thr	Gly	Gly	Thr	Gln	Thr	Ala	Ser	Asn	Thr	Ala	Gly	Asp	
465				470					475						480	
GCC	AAT	GGC	AAA	ACA	AAA	AAC	TAT	GAA	GTC	GAA	GTC	TGC	TGT	TCC	AAC	1488
Ala	Asn	Gly	Lys	Thr	Lys	Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	
			485					490						495		
CTC	AAT	TAT	CTG	AAA	TAC	GGG	TTG	CTG	ACG	CGC	AAA	ACT	GCC	GGC	AAC	1536
Leu	Asn	Tyr	Leu	Lys	Tyr	Gly	Leu	Leu	Thr	Arg	Lys	Thr	Ala	Gly	Asn	
			500				505						510			
ACG	GTG	GGA	AGC	GGC	AAC	AGC	AGC	CCA	ACC	GCC	GCC	GCC	CAA	ACG	GAC	1584
Thr	Val	Gly	Ser	Gly	Asn	Ser	Ser	Pro	Thr	Ala	Ala	Ala	Gln	Thr	Asp	
		515					520					525				

Glu	Val	Lys	Asp	Tyr	Lys	Asn	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	
125					130					135					140	
Tyr	Lys	His	Ala	Glu	Ser	Glu	Arg	Glu	Phe	Ser	Lys	Ile	Lys	Phe	Lys	
				145					150					155		
Ser	Gly	Asp	Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Lys	Asp	Pro	Ser	Arg	
			160					165					170			
Gln	Leu	Pro	Thr	Ser	Glu	Lys	Val	Ile	Tyr	Lys	Gly	Val	Trp	His	Phe	
		175					180					185				
Val	Thr	Asp	Thr	Glu	Lys	Gly	Gln	Lys	Phe	Asn	Asp	Ile	Leu	Glu	Thr	
	190					195					200					
Ser	Lys	Gly	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	Asp	Gly	
205					210					215					220	
Glu	Thr	Thr	Ser	Asn	Arg	Thr	Asp	Ser	Asn	Leu	Asn	Asp	Lys	His	Glu	
				225					230					235		
Gly	Tyr	Gly	Phe	Thr	Ser	Asn	Leu	Glu	Val	Asp	Phe	Gly	Ser	Lys	Lys	
			240					245					250			
Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Arg	Val	Thr	Asn	Ala	Thr	Thr	
		255					260					265				
Asn	Asp	Lys	Tyr	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	Gln	Ile	Thr	
	270					275					280					
Gly	Asn	Arg	Phe	Asn	Gly	Lys	Ala	Ile	Ala	Thr	Asp	Lys	Pro	Asp	Thr	
285					290					295					300	
Gly	Gly	Thr	Lys	Leu	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	
				305					310					315		
Gly	Gly	Phe	Phe	Gly	Pro	Lys	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	
			320					325					330			
Ser	Asp	Asp	Lys	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp	
		335					340					345				
Lys	Thr	Glu	Asn	Gly	Ala	Val	Ala	Ser	Gly	Gly	Thr	Asp	Ala	Ala	Ala	
	350					355					360					
Ser	Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys	Leu	Thr	Thr	
365					370					375					380	
Val	Leu	Asp	Ala	Val	Glu	Leu	Lys	Leu	Gly	Asp	Lys	Glu	Val	Gln	Lys	
				385					390					395		
Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	
			400					405					410			

Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Asn Asn Gln Ala Asn
 415 420 425
 Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr
 430 435 440
 Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly
 445 450 455 460
 Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys
 465 470 475
 Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
 480 485 490
 Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu
 495 500 505
 Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly Gln Ser Met
 510 515 520
 Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln
 525 530 535 540
 Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Ser Ser Thr
 545 550 555
 Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu
 560 565 570
 Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly Thr Leu Thr Ala
 575 580 585
 Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly
 590 595 600
 Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu Gly Phe Asp Leu
 605 610 615 620
 Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala
 625 630 635
 Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly
 640 645 650
 Trp Phe Ala Tyr Gln Gly Asp Lys Gln Thr Glu Asn Thr Thr Val Ala
 655 660 665
 Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala
 670 675 680
 Lys Arg Gln Lys Pro Val Gln
 685 690

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly
1 5 10 15
Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn Gly Lys
20 25 30
Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Ser Gly Gly Lys Glu
35 40 45
Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
50 55 60
Gly Ile Met Ile Pro Leu Leu Pro Lys Asn Ser Glu Ser Glu Ser Asn
65 70 75 80
Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
85 90 95
Glu His Thr Pro Glu Ser Asp Lys Lys Asp Thr Gln Ala Gly Thr Ala
100 105 110
Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
115 120 125
Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
130 135 140
Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145 150 155 160
Ala Gly Glu Asn Gly Ser Leu Ala Asp Ala Lys Thr Glu Gln Val Glu
165 170 175
Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
180 185 190
Lys Glu Gln Gln Asp Ile Val
195

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
1 5 10 15
Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
20 25 30
Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu
35 40 45
Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
50 55 60
Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Asn Asn
65 70 75 80
Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
85 90 95
Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
100 105 110
Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
115 120 125
Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
130 135 140
Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
145 150 155 160
Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
165 170 175
Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
180 185 190
Ser Glu Gln Asn Ile Val
195

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Lys Asp Asn Thr Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
1 5 10 15
Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
20 25 30
Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
35 40 45
Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
50 55 60
Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly
65 70 75 80
Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg
85 90 95
Lys Phe Ala His Thr Pro Lys Ser Asp Glu Lys Asp Thr His Ala Gly
100 105 110
Thr Ala Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr
115 120 125
Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
130 135 140
Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
145 150 155 160
Gly Glu Gly Gly Asn Gly Ser Gln Thr Ala Ala Ala Gln Thr Ala Gln
165 170 175
Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu
180 185 190
Ile Pro Ser Glu Gln Asn Val
195

GCG Ala 530	CAG Gln	AGT Ser	ATG Met	TTC Phe	CTC Leu	CAA Gln 535	GGC Gly	GAG Glu	CGC Arg	ACC Thr 540	GAT Asp 540	GAA Glu	AAC Asn	AAG Lys	ATT Ile	1632
CCA Pro 545	AGC Ser	GAG Glu	CAA Gln	AAC Asn	GTC Val 550	GTT Val	TAT Tyr	CGG Arg	GGG Gly	TCT Ser 555	TGG Trp	TAC Tyr	GGG Gly	CAT His	ATT Ile 560	1680
GCC Ala	AGC Ser	AGC Ser	ACA Thr	AGC Ser 565	TGG Trp	AGC Ser	GGC Gly	AAT Asn	GCT Ala 570	TCT Ser	GAT Asp	AAA Lys	GAG Glu	GGC Gly 575	GGC Gly	1728
AAC Asn	AGG Arg	GCG Ala	GAA Glu 580	TTT Phe	ACT Thr	GTG Val	AAT Asn	TTT Phe 585	GGC Gly	GAG Glu	AAA Lys	AAA Lys	ATT Ile 590	ACC Thr	GGC Gly	1776
ACG Thr	TTA Leu	ACC Thr 595	GCT Ala	GAA Glu	AAC Asn	AGG Arg	CAG Gln 600	GAG Glu	GCA Ala	ACC Thr	TTT Phe 605	ACC Thr	ATT Ile	GAT Asp	GGT Gly	1824
AAG Lys 610	ATT Ile	GAG Glu	GGC Gly	AAC Asn	GGT Gly	TTT Phe 615	TCC Ser	GGT Gly	ACG Thr	GCA Ala	AAA Lys 620	ACT Thr	GCT Ala	GAA Glu	TTA Leu	1872
GGT Gly 625	TTT Phe	GAT Asp	CTC Leu	GAT Asp	CAA Gln 630	AAA Lys	AAT Asn	ACC Thr	ACC Thr	CGC Arg 635	ACG Thr	CCT Pro	AAG Lys	GCA Ala	TAT Tyr 640	1920
ATC Ile	ACA Thr	GAT Asp	GCC Ala	AAG Lys 645	GTA Val	AAG Lys	GGC Gly	GGT Gly	TTT Phe 650	TAC Tyr	GGG Gly	CCC Pro	AAA Lys	GCC Ala 655	GAA Glu	1968
GAG Glu	TTG Leu	GGC Gly	GGA Gly	TGG Trp	TTT Phe	GCC Ala	TAT Tyr	TCG Ser 665	GAC Asp	GAT Asp	AAA Lys	CAA Gln	ACG Thr 670	AAA Lys	AAT Asn	2016
GCA Ala	ACA Thr	GAT Asp 675	GCA Ala	TCC Ser	GGC Gly	AAT Asn 680	GGA Gly	AAT Asn	TCA Ser	GCA Ala	AGC Ser	AGT Ser	GCA Ala	ACT Thr	GTC Val	2064
GTA Val 690	TTC Phe	GGT Gly	GCG Ala	AAA Lys	CGC Arg 695	CAA Gln	CAG Gln	CCT Pro	GTG Val	CAA Gln	TAAACCAAGG	CGGATAC				2114

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Leu Gly Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr
1 5 10 15
Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys
20 25 30
Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu
35 40 45
Lys Arg Arg Asn Trp Tyr Pro Ser Ala Lys Glu Asn Glu Val Lys Leu
50 55 60
Asn Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Ser Asn Pro Lys Asn
65 70 75 80
Leu Pro Glu Arg Gln Lys Ser Val Ile Asp Gln Val Glu Thr Asp Gly
85 90 95
Asp Ser Asn Asn Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser
100 105 110
Asn His Gln Asn Gly Asn Thr Gly Asn Gly Val Asn Gln Pro Lys Asn
115 120 125
Glu Val Thr Asp Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe
130 135 140
Tyr Lys His Ala Lys Arg Glu Val Asn Leu Ala Val Glu Pro Lys Ile
145 150 155 160
Ala Lys Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro
165 170 175
Ser Arg Gln Leu Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp
180 185 190
His Phe Ala Thr Asp Thr Lys Arg Gly Gln Lys Phe Arg Glu Ile Ile
195 200 205
Gln Pro Ser Lys Asn Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp
210 215 220
Asp Asp Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly
225 230 235 240
His Glu Gly Tyr Gly Phe Ala Ser Asn Leu Glu Val Asp Phe Asp Asn
245 250 255
Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Asn Gln Asn Asn
260 265 270

Asn	Thr	Asn	Asn	Asp	Lys	His	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	
		275					280					285				
Thr	Leu	Lys	Gly	Asn	Arg	Phe	Ser	Gly	Lys	Ala	Glu	Ala	Thr	Asp	Lys	
	290					295					300					
Pro	Lys	Asn	Asp	Gly	Glu	Thr	Lys	Glu	His	Pro	Phe	Val	Ser	Asp	Ser	
305					310					315					320	
Ser	Ser	Leu	Ser	Gly	Gly	Phe	Phe	Gly	Pro	Gln	Gly	Glu	Glu	Leu	Gly	
				325					330					335		
Phe	Arg	Phe	Leu	Ser	Asn	Asp	Gln	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	
			340					345					350			
Lys	Thr	Lys	Asp	Lys	Pro	Ala	Asn	Gly	Asn	Thr	Ala	Glu	Ala	Ser	Gly	
		355					360					365				
Gly	Thr	Asp	Ala	Ala	Ala	Ser	Gly	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	
	370					375					380					
Asn	Ser	Lys	Leu	Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	Thr	His	Gly	
385					390					395					400	
Gly	Thr	Ala	Ile	Lys	Asn	Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	
			405						410					415		
Val	Val	Asp	Gly	Ile	Met	Ile	Pro	Leu	Leu	Pro	Gln	Asn	Ser	Thr	Gly	
			420					425					430			
<i>Cont.</i> Lys	Asn	Asn	Gln	Pro	Asp	Gln	Gly	Lys	Asn	Gly	Gly	Thr	Ala	Phe	Ile	
		435					440					445				
Tyr	Lys	Thr	Thr	Tyr	Thr	Pro	Lys	Asn	Asp	Asp	Lys	Asp	Thr	Lys	Ala	
	450					455					460					
Gln	Thr	Val	Thr	Gly	Gly	Thr	Gln	Thr	Ala	Ser	Asn	Thr	Ala	Gly	Asp	
465					470					475					480	
Ala	Asn	Gly	Lys	Thr	Lys	Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	
				485					490					495		
Leu	Asn	Tyr	Leu	Lys	Tyr	Gly	Leu	Leu	Thr	Arg	Lys	Thr	Ala	Gly	Asn	
			500					505					510			
Thr	Val	Gly	Ser	Gly	Asn	Ser	Ser	Pro	Thr	Ala	Ala	Ala	Gln	Thr	Asp	
		515					520					525				
Ala	Gln	Ser	Met	Phe	Leu	Gln	Gly	Glu	Arg	Thr	Asp	Glu	Asn	Lys	Ile	
	530					535					540					
Pro	Ser	Glu	Gln	Asn	Val	Val	Tyr	Arg	Gly	Ser	Trp	Tyr	Gly	His	Ile	
545					550					555					560	

Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly
565 570 575

Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly
580 585 590

Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly
595 600 605

Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu
610 615 620

Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr
625 630 635 640

Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu
645 650 655

Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn
660 665 670

Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val
675 680 685

Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln
690 695

(2) INFORMATION FOR SEQ ID NO:11:

B1
cont. (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: IM2169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly
1 5 10 15

Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
35 40 45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr
 65 70 75 80
 Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe
 85 90 95
 Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
 100 105 110
 Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
 115 120 125
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160
 Ala Gly Gly Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190
 Thr Asp Gln Asn Val Val
 195

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 6940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
 1 5 10 15
 Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
 20 25 30
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu
 35 40 45

Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
 65 70 75 80
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95
 Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
 100 105 110
 Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
 115 120 125
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190
 Ser Glu Gln Asn Ile Val
 195

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: 2223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp
 1 5 10 15
 Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys
 20 25 30
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu
 35 40 45

Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn
 65 70 75 80
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95
 Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln
 100 105 110
 Ala Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly
 115 120 125
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190
 Ser Glu Gln Asn Ile Val
 195

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: C708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Gln Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Thr Gly
 1 5 10 15
 Ala Ala Arg Ser Asn Gly Ala Ala Gly Gln Ser Ser Glu Asn Ser Lys
 20 25 30
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
 35 40 45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp
 50 55 60
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Lys Asn
 65 70 75 80
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
 85 90 95
 Asn His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala
 100 105 110
 Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly
 115 120 125
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr
 130 135 140
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln
 145 150 155 160
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro
 180 185 190
 Asn Asp Gln Asn Val Val
 195

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: M978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Gln Asp Lys Ala Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly
 1 5 10 15
 Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
 20 25 30
 Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp
 35 40 45

Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
 50 55 60
 Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly
 65 70 75 80
 Ser Asn Gln Ala Asp Lys Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly
 85 90 95
 Gly Thr Asp Phe Thr Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp
 100 105 110
 Lys Asp Thr Lys Ala Gln Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln
 115 120 125
 Thr Asp Leu Gly Lys Ala Asp Val Asn Gly Gly Lys Ala Glu Thr Lys
 130 135 140
 Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr
 145 150 155 160
 Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly
 165 170 175
 Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met
 180 185 190
 Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln
 195 200 205
 Asn Val Val
 210

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 1610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys Arg Asp Lys Ala Glu Ser Gly Gly Gly Asn Gly Ala Ser Gly Gly
 1 5 10 15
 Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn
 20 25 30

Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Gly Lys
20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys
35 40 45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Ala
50 55 60

Gly Ile Met Ile Pro Leu Met Pro Glu Thr Ser Glu Ser Gly Asn Asn
65 70 75 80

Gln Ala Asp Leu Gly Leu Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe
85 90 95

Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Pro
100 105 110

Thr Asn Gly Ala Gln Thr Ala Ser Gly Thr Ala Gly Val Thr Gly Gly
115 120 125

Gln Ala Gly Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn
130 135 140

Tyr Leu Lys Thr Gly Leu Leu Thr Arg Lys Thr Ala Asp Asn Thr Val
145 150 155 160

Gly Ser Gly Asn Gly Ser Ser Thr Ala Ala Ala Gln Thr Ala Gln Gly
165 170 175

Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile
180 185 190

Pro Lys Glu Gln Gln Asp Ile Val
195 200

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: S3032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly
 1 5 10 15
 Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn
 20 25 30
 Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly
 35 40 45
 Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val
 50 55 60
 Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly Lys
 65 70 75 80
 Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile Tyr
 85 90 95
 Leu Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln
 100 105 110
 Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp Ala
 115 120 125
 Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu
 130 135 140
 Asn Tyr Leu Lys Thr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr
 145 150 155 160
 Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp Ala
 165 170 175
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro
 180 185 190
 Ser Glu Gln Asn Val Val
 195

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Thr Lys Asp Lys Pro Gly Asn Gly Ala Arg Leu Gln Ala Ala Arg Cys
1 5 10 15
Gly Thr Ser Asn Gly Ala Ala Gly Gln Ser Ser Glu Asn Ser Lys Leu
20 25 30
Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val
35 40 45
Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly
50 55 60
Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Lys Asn Gln
65 70 75 80
Ala Asp Lys Gly Lys Asn Gly Glu Thr Glu Phe Thr Arg Lys Phe Glu
85 90 95
His Thr Pro Glu Ser Asp Glu Lys Asp Ala Gln Ala Gly Thr Pro Ser
100 105 110
Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys
115 120 125
Thr Lys Thr Tyr Glu Val Asn Leu Cys Ser Asn Leu Asn Tyr Leu Lys
130 135 140
Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly Glu Gly Gly
145 150 155 160
Asn Ser Ser Pro Thr Ala Ala Gln Thr Ala Gln Gly Ala Gln Ser Met
165 170 175
Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln
180 185 190
Asn Val Val
195

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AAACCCGGAT CCGTTGCCAG CGCTGCCGT

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTTTCATG AGATATCTGG CAACATTGTT GTTATCTCTG GCGGTGTTAA TCACCGCCGG 60
GTGCCTGGGT GGC GGCGGCA GTTTC 85

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTGTTTTTGT TGAGTGCATG CCTGGGTGGC 30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGCGCAAGCT TACAGTTTGT CTTTGGTTTT CGCGCTGCCG 40

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAAAGCATG CATAAAACT ACGCGTTACA CCATTCAAGC

40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

B'
cat (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TATATAAGCT TACGTTGCAG GCCCTGCCGC GTTTTCCCC

39

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCCGAATTCT GCCGTCTGAA GCCTTATTC

29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCCGAATTCT GCTATGGTGC TGCCTGTG

28

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGCATCCAAA ACCGTACCTG TGCTGCCTGA

30

(2) INFORMATION FOR SEQ ID NO:29:

B' cont.
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTATCACTT TCCGGGGGCA GGAGCGGAAT

30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTTGGAACAG CAGACAGCGG TTTGCGCCCC

30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAACATACTT TGTTCGTTTT TGC GCGTCAA

30

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

b'
cont. (vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Tyr Lys Gly Thr Trp
1 5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly Thr Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- B' cont.
- (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala Val Phe Gly Ala Lys
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2067

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 1..60

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 61..2067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT	48
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	
-20 -15 -10 -5	
TTG TTG AGT GCT TGT CTG GGC GGA GGC GGC AGT TTC GAT CTT GAT TCT	96
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser	
1 5 10	
GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT	144
Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser	
15 20 25	
TCC GAA ACA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCA	192
Ser Glu Thr Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala	
30 35 40	
ATG CGC TTC AAG CGG CGG AAT TGG TAC CCA AAA AAT GAA GAA GAT CAT	240
Met Arg Phe Lys Arg Arg Asn Trp Tyr Pro Lys Asn Glu Glu Asp His	
45 50 55 60	
AAG GCA TTA TCA GAA GCG GAT TGG GAG AAG TTA GGT GCG GGT AAG CCA	288
Lys Ala Leu Ser Glu Ala Asp Trp Glu Lys Leu Gly Ala Gly Lys Pro	
65 70 75	
GAT GAG TTT CCC CAA AGG AAT GAA ATA TTG AAT ATG ACT GAC GGA ATT	336
Asp Glu Phe Pro Gln Arg Asn Glu Ile Leu Asn Met Thr Asp Gly Ile	
80 85 90	
CTG AGT GAG TCT CTT CAG CTG GGT GAG GGC GGC AAA AGC CGC GTA GAA	384
Leu Ser Glu Ser Leu Gln Leu Gly Glu Gly Gly Lys Ser Arg Val Glu	
95 100 105	
GGA TAC ACG GAT TTC CAA TAT GTC CGC TCG GGC TAT ATC TAC CGC AAC	432
Gly Tyr Thr Asp Phe Gln Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Asn	
110 115 120	

GGT Gly 125	GCC Ala	AAT Asn	AAA Lys	ATC Ile	GAT Asp 130	TTC Phe	CAA Gln	AAA Lys	AAA Lys	ATC Ile 135	GCC Ala	CTT Leu	TCC Ser	GGT Gly	CCG Pro 140	480
GAC Asp	GGC Gly	TAC Tyr	CTT Leu	TTC Phe 145	TAC Tyr	AAA Lys	GGC Gly	AGC Ser	AAT Asn 150	CCT Pro	TCC Ser	CAA Gln	GCT Ala	CTG Leu 155	CCG Pro	528
ATG Met	GGT Gly	AAG Lys	GTA Val 160	GGT Gly	TAT Tyr	AAA Lys	GGT Gly	ACT Thr 165	TGG Trp	GAT Asp	TAT Tyr	GTA Val	ACC Thr 170	GAT Asp	GCC Ala	576
AAG Lys	ATG Met	GGA Gly 175	CAA Gln	AAA Lys	TTT Phe	TCC Ser	CAG Gln 180	TTG Leu	GCT Ala	GGT Gly	TTT Phe	CCA Pro 185	GCG Ala	GGG Gly	GAT Asp	624
AGG Arg 190	TAT Tyr	GGG Gly	GCT Ala	TTG Leu	TCT Ser	GCC Ala 195	GAG Glu	GAA Glu	GCG Ala	GAT Asp	GTG Val 200	TTG Leu	CGC Arg	AAC Asn	AAA Lys	672
AGC Ser 205	GAG Glu	GCA Ala	CAG Gln	CAA Gln 210	GGT Gly	CAG Gln	ACC Thr	GAT Asp	TTC Phe	GGG Gly 215	CTG Leu	ACC Thr	AGC Ser	GAG Glu	TTT Phe 220	720
GAG Glu	GTG Val	GAT Asp	TTC Phe 225	GCC Ala	GCC Ala	AAG Lys	ACC Thr	ATG Met	ACC Thr 230	GGC Gly	GCG Ala	CTC Leu	TAC Tyr	CGC Arg 235	AAT Asn	768
AAC Asn	CGG Arg	ATT Ile	ACT Thr 240	AAT Asn	AAC Asn	GAA Glu	ACC Thr	GAA Glu 245	AAT Asn	AAA Lys	GCC Ala	AAA Lys	CAA Gln 250	ATT Ile	AAA Lys	816
CGT Arg	TAC Tyr	GAC Asp 255	ATT Ile	CAG Gln	GCT Ala	GAC Asp	CTG Leu 260	CAC His	GGT Gly	AAC Asn	CGC Arg	TTC Phe 265	AGC Ser	GGC Gly	AAG Lys	864
GCA Ala 270	ACG Thr	GCA Ala	ACC Thr	GAC Asp	AAA Lys	CCC Pro 275	AAA Lys	AAC Asn	GAC Asp	GAA Glu	ACC Thr 280	AAG Lys	GAA Glu	CAT His	CCC Pro	912
TTT Phe 285	GTT Val	TCC Ser	GAC Asp	TCG Ser 290	TCT Ser	TCT Ser	TTG Leu	AGC Ser	GGC Gly	GGC Gly 295	TTT Phe	TTC Phe	GGT Gly	CCG Pro 300	AAG Lys	960
GGT Gly	GAG Glu	GAA Glu	TTG Leu 305	GGT Gly	TTC Phe	CGC Arg	TTT Phe	TTG Leu 310	AGC Ser	GAC Asp	GAT Asp	CAA Gln	AAA Lys	GTT Val 315	GCC Ala	1008
GTT Val	GTC Val	GCC Gly 320	AGC Ser	GCG Ala	AAA Lys	ACC Thr	AAA Lys	GAC Asp 325	AAA Lys	CTG Leu	GAA Glu	AAT Asn	GGC Gly 330	GCG Ala	GCG Ala	1056

8' only.

GCT	TCA	GGC	AGC	ACA	GGT	GCG	GCA	GCA	TCG	GGC	GGT	GCG	GCA	GAT	ATG	1104
Ala	Ser	Gly	Ser	Thr	Gly	Ala	Ala	Ala	Ser	Gly	Gly	Ala	Ala	Asp	Met	
		335						340					345			
CCG	TCT	GAA	AAC	GGT	AAG	CTG	ACC	ACG	GTT	TTG	GAT	GCG	GTT	GAG	CTG	1152
Pro	Ser	Glu	Asn	Gly	Lys	Leu	Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	
		350				355					360					
AAA	TCT	GGC	GGT	AAG	GAA	GTC	AAA	AAT	CTC	GAC	AAC	TTC	AGC	AAT	GCC	1200
Lys	Ser	Gly	Gly	Lys	Glu	Val	Lys	Asn	Leu	Asp	Asn	Phe	Ser	Asn	Ala	
		365			370					375					380	
GCC	CAA	CTG	GTT	GTC	GAC	GGC	ATT	ATG	ATT	CCG	CTC	CTG	CCC	AAG	AAT	1248
Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	Ile	Pro	Leu	Leu	Pro	Lys	Asn	
				385					390					395		
TCC	GAA	AGC	GAG	AGC	AAT	CAG	GCA	GAT	AAA	GGT	AAA	AAC	GGC	GGA	ACA	1296
Ser	Glu	Ser	Glu	Ser	Asn	Gln	Ala	Asp	Lys	Gly	Lys	Asn	Gly	Gly	Thr	
			400					405					410			
GCC	TTT	ACC	CGC	AAA	TTT	GAA	CAC	ACG	CCG	GAA	AGT	GAT	AAA	AAA	GAC	1344
Ala	Phe	Thr	Arg	Lys	Phe	Glu	His	Thr	Pro	Glu	Ser	Asp	Lys	Lys	Asp	
		415					420					425				
ACC	CAA	GCA	GGT	ACG	GCG	GAG	AAT	GGC	AAT	CCA	GCC	GCT	TCA	AAT	ACG	1392
Thr	Gln	Ala	Gly	Thr	Ala	Glu	Asn	Gly	Asn	Pro	Ala	Ala	Ser	Asn	Thr	
		430				435					440					
GCA	GGT	GAT	ACC	AAT	GGC	AAA	ACA	AAA	ACC	TAT	GAA	GTC	GAA	GTC	TGC	1440
Ala	Gly	Asp	Thr	Asn	Gly	Lys	Thr	Lys	Thr	Tyr	Glu	Val	Glu	Val	Cys	
		445			450					455					460	
TGT	TCC	AAC	CTC	AAT	TAT	CTG	AAA	TAC	GGA	ATG	TTG	ACG	CGT	AAA	AAC	1488
Cys	Ser	Asn	Leu	Asn	Tyr	Leu	Lys	Tyr	Gly	Met	Leu	Thr	Arg	Lys	Asn	
				465					470					475		
AGC	AAG	TCC	GCG	ATG	CAG	GCA	GGC	GAA	AAC	GGT	AGT	CTA	GCT	GAC	GCT	1536
Ser	Lys	Ser	Ala	Met	Gln	Ala	Gly	Glu	Asn	Gly	Ser	Leu	Ala	Asp	Ala	
			480					485					490			
AAA	ACG	GAA	CAA	GTT	GAA	CAA	AGT	ATG	TTC	CTC	CAA	GGC	GAG	CGC	ACC	1584
Lys	Thr	Glu	Gln	Val	Glu	Gln	Ser	Met	Phe	Leu	Gln	Gly	Glu	Arg	Thr	
		495					500					505				
GAT	GAA	AAA	GAG	ATT	CCA	AAA	GAG	CAA	CAA	GAC	ATC	GTT	TAT	CGG	GGG	1632
Asp	Glu	Lys	Glu	Ile	Pro	Lys	Glu	Gln	Gln	Asp	Ile	Val	Tyr	Arg	Gly	
		510				515					520					
TCT	TGG	TAC	GGG	CAT	ATT	GCC	AAC	GAC	ACA	AGC	TGG	AGC	GGC	AAT	GCT	1680
Ser	Trp	Tyr	Gly	His	Ile	Ala	Asn	Asp	Thr	Ser	Trp	Ser	Gly	Asn	Ala	
					530					535					540	

TCA	GAT	AGA	GAG	GGC	GGC	AAC	AGG	GCG	GAC	TTT	ACC	GTG	AAT	TTT	GGT	1728
Ser	Asp	Arg	Glu	Gly	Gly	Asn	Arg	Ala	Asp	Phe	Thr	Val	Asn	Phe	Gly	
			545						550					555		
ACG	AAA	AAA	ATT	AAC	GGA	ACG	TTA	ACC	GCT	GAA	AAC	AGG	CAG	GAG	GCA	1776
Thr	Lys	Lys	Ile	Asn	Gly	Thr	Leu	Thr	Ala	Glu	Asn	Arg	Gln	Glu	Ala	
			560					565					570			
ACC	TTT	ACC	ATT	GTG	GGC	GAT	ATT	AAG	GAC	AAC	GGC	TTT	GAA	GGT	ACG	1824
Thr	Phe	Thr	Ile	Val	Gly	Asp	Ile	Lys	Asp	Asn	Gly	Phe	Glu	Gly	Thr	
		575					580					585				
GCG	AAA	ACT	GCT	GAC	TCA	GGT	TTT	GAT	CTC	GAT	CAA	AGC	AAT	ACC	ACC	1872
Ala	Lys	Thr	Ala	Asp	Ser	Gly	Phe	Asp	Leu	Asp	Gln	Ser	Asn	Thr	Thr	
	590					595					600					
CGC	ACG	CCT	AAG	GCA	TAT	ATC	ACA	GAT	GCC	AAG	GTG	AAG	GGC	GGT	TTT	1920
Arg	Thr	Pro	Lys	Ala	Tyr	Ile	Thr	Asp	Ala	Lys	Val	Lys	Gly	Gly	Phe	
605					610					615					620	
TAC	GGG	CCT	AAA	GCC	GAA	GAG	TTG	GGC	GGA	TGG	TTT	GCC	TAT	CCG	GGC	1968
Tyr	Gly	Pro	Lys	Ala	Glu	Glu	Leu	Gly	Gly	Trp	Phe	Ala	Tyr	Pro	Gly	
				625					630					635		
GAT	AAA	CAA	ACG	GAA	AAG	GCA	ACG	GTT	ACA	TCC	GGC	GAT	GGA	AAT	TCA	2016
Asp	Lys	Gln	Thr	Glu	Lys	Ala	Thr	Val	Thr	Ser	Gly	Asp	Gly	Asn	Ser	
			640					645					650			
GCA	AGC	AGT	GCA	ACT	GTC	GTA	TTC	GGT	GCG	AAA	CGC	CAA	AAG	CCT	GTG	2064
Ala	Ser	Ser	Ala	Thr	Val	Val	Phe	Gly	Ala	Lys	Arg	Gln	Lys	Pro	Val	
		655					660					665				
CAA	TAAAGTTTCG	ATCTTGATTC	TGTCGATACC	GAAGCCCCGC	GTCCCGCGCC	AAATAAAA	2125									
Gln																

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Asn	Asn	Pro	Leu	Val	Asn	Gln	Ala	Ala	Met	Val	Leu	Pro	Val	Phe	
-20					-15					-10					-5	
Leu	Leu	Ser	Ala	Cys	Leu	Gly	Gly	Gly	Gly	Ser	Phe	Asp	Leu	Asp	Ser	
				1				5					10			

Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser
 15 20 25
 Ser Glu Thr Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala
 30 35 40
 Met Arg Phe Lys Arg Arg Asn Trp Tyr Pro Lys Asn Glu Glu Asp His
 45 50 55 60
 Lys Ala Leu Ser Glu Ala Asp Trp Glu Lys Leu Gly Ala Gly Lys Pro
 65 70 75
 Asp Glu Phe Pro Gln Arg Asn Glu Ile Leu Asn Met Thr Asp Gly Ile
 80 85 90
 Leu Ser Glu Ser Leu Gln Leu Gly Glu Gly Gly Lys Ser Arg Val Glu
 95 100 105
 Gly Tyr Thr Asp Phe Gln Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Asn
 110 115 120
 Gly Ala Asn Lys Ile Asp Phe Gln Lys Lys Ile Ala Leu Ser Gly Pro
 125 130 135 140
 Asp Gly Tyr Leu Phe Tyr Lys Gly Ser Asn Pro Ser Gln Ala Leu Pro
 145 150 155
 Met Gly Lys Val Gly Tyr Lys Gly Thr Trp Asp Tyr Val Thr Asp Ala
 160 165 170
 Lys Met Gly Gln Lys Phe Ser Gln Leu Ala Gly Phe Pro Ala Gly Asp
 175 180 185
 Arg Tyr Gly Ala Leu Ser Ala Glu Glu Ala Asp Val Leu Arg Asn Lys
 190 195 200
 Ser Glu Ala Gln Gln Gly Gln Thr Asp Phe Gly Leu Thr Ser Glu Phe
 205 210 215 220
 Glu Val Asp Phe Ala Ala Lys Thr Met Thr Gly Ala Leu Tyr Arg Asn
 225 230 235
 Asn Arg Ile Thr Asn Asn Glu Thr Glu Asn Lys Ala Lys Gln Ile Lys
 240 245 250
 Arg Tyr Asp Ile Gln Ala Asp Leu His Gly Asn Arg Phe Ser Gly Lys
 255 260 265
 Ala Thr Ala Thr Asp Lys Pro Lys Asn Asp Glu Thr Lys Glu His Pro
 270 275 280
 Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Lys
 285 290 295 300

Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln Lys Val Ala
 305 310 315
 Val Val Gly Ser Ala Lys Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala
 320 325 330
 Ala Ser Gly Ser Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met
 335 340 345
 Pro Ser Glu Asn Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu
 350 355 360
 Lys Ser Gly Gly Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala
 365 370 375 380
 Ala Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asn
 385 390 395
 Ser Glu Ser Glu Ser Asn Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr
 400 405 410
 Ala Phe Thr Arg Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp
 415 420 425
 Thr Gln Ala Gly Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr
 430 435 440
 Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys
 445 450 455 460
 Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn
 465 470 475
 Ser Lys Ser Ala Met Gln Ala Gly Glu Asn Gly Ser Leu Ala Asp Ala
 480 485 490
 Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr
 495 500 505
 Asp Glu Lys Glu Ile Pro Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly
 510 515 520
 Ser Trp Tyr Gly His Ile Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala
 525 530 535 540
 Ser Asp Arg Glu Gly Gly Asn Arg Ala Asp Phe Thr Val Asn Phe Gly
 545 550 555
 Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala
 560 565 570
 Thr Phe Thr Ile Val Gly Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr
 575 580 585

Ala Lys Thr Ala Asp Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr
590 595 600

Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe
605 610 615 620

Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly
625 630 635

Asp Lys Gln Thr Glu Lys Ala Thr Val Thr Ser Gly Asp Gly Asn Ser
640 645 650

Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Lys Pro Val
655 660 665

Gln

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2133

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..60

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 61..2133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT	48
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	
-20 -15 -10 -5	
TTG TTG AGT GCT TGT TTG GGC GGA GGC GGC AGT TTC GAT CTT GAT TCT	96
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser	
1 5 10	

GTC Val	GAT Asp	ACC Thr 15	GAA Glu	GCC Ala	CCG Pro	CGT Arg	CCC Pro 20	GCG Ala	CCA Pro	AAA Lys	TAT Tyr	CAA Gln 25	GAT Asp	GTT Val	TCT Ser	144
TCC Ser	GAA Glu 30	AAA Lys	CCG Pro	CAA Gln	GCC Ala	CAA Gln 35	AAA Lys	GAC Asp	CAA Gln	GGC Gly	GGA Gly 40	TAC Tyr	GGT Gly	TTT Phe	GCG Ala	192
ATG Met 45	AGG Arg	TTG Leu	AAA Lys	CGG Arg	AGG Arg 50	AAT Asn	CGG Arg	CAT His	CCG Pro	CAG Gln 55	GCA Ala	AAA Lys	GAA Glu	GAC Asp	AAA Lys 60	240
GTT Val	GAA Glu	CTA Leu	AAC Asn	CCA Pro 65	AAT Asn	GAT Asp	TGG Trp	GAG Glu	GAG Glu 70	ACA Thr	GGA Gly	TTG Leu	CCG Pro	AGC Ser 75	AAG Lys	288
CCC Pro	CAA Gln	AAC Asn 80	TTA Leu	CCC Pro	GAG Glu	CGA Arg	CAG Gln 85	CAA Gln	TCG Ser	GTT Val	ATT Ile	GAT Asp 90	AAA Lys	GTA Val	AAA Lys	336
ACA Thr	GAC Asp 95	GAT Asp	GGC Gly	AGC Ser	AAT Asn	ATT Ile 100	TAC Tyr	ACT Thr	TCC Ser	CCT Pro	TAT Tyr 105	CTC Leu	ACG Thr	CAA Gln	TCA Ser	384
AAC Asn 110	CAT His	CAA Gln	AAC Asn	GGC Gly	AGC Ser	ACT Thr 115	AAT Asn	AGC Ser	GGT Gly	GCA Ala	AAC Asn 120	CAA Gln	CCA Pro	AAA Lys	AAC Asn	432
GAA Glu 125	GTA Val	AAA Lys	GAT Asp	TAC Tyr	AAA Lys 130	AAT Asn	TTC Phe	AAA Lys	TAT Tyr	GTT Val 135	TAT Tyr	TCC Ser	GGC Gly	TGG Trp	TTT Phe 140	480
TAT Tyr	AAA Lys	CAT His	GCA Ala	GAG Glu 145	AGT Ser	GAA Glu	AGA Arg	GAA Glu	TTC Phe 150	AGT Ser	AAA Lys	ATC Ile	AAA Lys	TTT Phe 155	AAG Lys	528
TCA Ser	GGC Gly	GAC Asp 160	GAC Asp	GGC Gly	TAT Tyr	ATT Ile	TTT Phe 165	TAT Tyr	CAC His	GGT Gly	AAA Lys	GAC Asp 170	CCT Pro	TCC Ser	CGA Arg	576
CAA Gln	CTT Leu 175	CCC Pro	ACT Thr	TCT Ser	GAA Glu	AAA Lys	GTT Val 180	ATC Ile	TAC Tyr	AAA Lys	GGC Gly 185	GTA Val	TGG Trp	CAT His	TTT Phe	624
GTA Val 190	ACC Thr	GAT Asp	ACT Thr	GAA Glu	AAG Lys	GGA Gly 195	CAA Gln	AAA Lys	TTT Phe	AAC Asn 200	GAT Asp	ATT Ile	CTT Leu	GAA Glu	ACC Thr	672
TCA Ser 205	AAA Lys	GGG Gly	CAA Gln	GGC Gly	GAC Asp 210	AGA Arg	TAC Tyr	AGC Ser	GGA Gly	TTT Phe 215	TCG Ser	GGC Gly	GAT Asp	GAC Asp	GGC Gly 220	720

GAA	ACA	ACT	TCC	AAT	AGA	ACT	GAT	TCC	AAC	CTT	AAT	GAT	AAG	CAC	GAG	768
Glu	Thr	Thr	Ser	Asn	Arg	Thr	Asp	Ser	Asn	Leu	Asn	Asp	Lys	His	Glu	
				225					230					235		
GGT	TAT	GGT	TTT	ACC	TCG	AAT	TTA	GAA	GTG	GAT	TTC	GGC	AGT	AAA	AAA	816
Gly	Tyr	Gly	Phe	Thr	Ser	Asn	Leu	Glu	Val	Asp	Phe	Gly	Ser	Lys	Lys	
			240					245					250			
TTG	ACG	GGT	AAA	TTA	ATA	CGC	AAT	AAT	AGA	GTT	ACA	AAC	GCT	ACT	ACT	864
Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Arg	Val	Thr	Asn	Ala	Thr	Thr	
		255					260					265				
AAC	GAT	AAA	TAC	ACC	ACC	CAA	TAC	TAC	AGC	CTT	GAT	GCC	CAA	ATA	ACA	912
Asn	Asp	Lys	Tyr	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	Gln	Ile	Thr	
	270					275					280					
GGC	AAC	CGC	TTC	AAC	GGT	AAG	GCG	ATA	GCG	ACC	GAC	AAA	CCC	GAC	ACT	960
Gly	Asn	Arg	Phe	Asn	Gly	Lys	Ala	Ile	Ala	Thr	Asp	Lys	Pro	Asp	Thr	
285				290					295						300	
GGA	GGA	ACC	AAA	CTA	CAT	CCC	TTT	GTT	TCC	GAC	TCG	TCT	TCT	TTG	AGC	1008
Gly	Gly	Thr	Lys	Leu	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	
				305				310						315		
GGC	GGC	TTT	TTC	GGT	CCG	AAG	GGT	GAG	GAA	TTG	GGT	TTC	CGC	TTT	TTG	1056
Gly	Gly	Phe	Phe	Gly	Pro	Lys	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	
			320					325					330			
AGC	GAC	GAT	AAA	AAA	GTT	GCG	GTT	GTC	GGC	AGC	GCG	AAA	ACC	AAA	GAC	1104
Ser	Asp	Asp	Lys	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp	
		335					340					345				
AAA	ACG	GAA	AAT	GGC	GCG	GTG	GCT	TCA	GGC	GGC	ACA	GAT	GCG	GCA	GCA	1152
Lys	Thr	Glu	Asn	Gly	Ala	Val	Ala	Ser	Gly	Gly	Thr	Asp	Ala	Ala	Ala	
	350					355					360					
TCA	AAC	GGT	GCG	GCA	GGC	ACG	TCG	TCT	GAA	AAC	AGT	AAG	CTG	ACC	ACG	1200
Ser	Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys	Leu	Thr	Thr	
365					370					375					380	
GTT	TTG	GAT	GCG	GTC	GAG	CTG	AAA	TTG	GGC	GAT	AAG	GAA	GTC	CAA	AAG	1248
Val	Leu	Asp	Ala	Val	Glu	Leu	Lys	Leu	Gly	Asp	Lys	Glu	Val	Gln	Lys	
				385					390					395		
CTC	GAC	AAC	TTC	AGC	AAC	GCC	GCC	CAA	CTG	GTT	GTC	GAC	GGC	ATT	ATG	1296
Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	
			400					405					410			
ATT	CCG	CTC	TTG	CCC	GAG	ACT	TCC	GAA	AGT	GGG	AAC	AAT	CAA	GCC	AAT	1344
Ile	Pro	Leu	Leu	Pro	Glu	Thr	Ser	Glu	Ser	Gly	Asn	Asn	Gln	Ala	Asn	
		415					420					425				

CAA Gln 430	GGT Gly 430	ACA Thr 430	AAT Asn 430	GGC Gly 430	GGA Gly 435	ACA Thr 435	GCC Ala 435	TTT Phe 435	ACC Thr 435	CGC Arg 440	AAA Lys 440	TTT Phe 440	GAC Asp 440	CAC His 440	ACG Thr 440	1392
CCG Pro 445	GAA Glu 445	AGT Ser 445	GAT Asp 445	AAA Lys 450	AAA Lys 450	GAC Asp 450	GCC Ala 450	CAA Gln 450	GCA Ala 455	GGT Gly 455	ACG Thr 455	CAG Gln 455	ACG Thr 455	AAT Asn 460	GGG Gly 460	1440
GCG Ala 465	CAA Gln 465	ACC Thr 465	GCT Ala 465	TCA Ser 465	AAT Asn 465	ACG Thr 465	GCA Ala 470	GGT Gly 470	GAT Asp 470	ACC Thr 470	AAT Asn 475	GGC Gly 475	AAA Lys 475	ACA Thr 475	AAA Lys 475	1488
ACC Thr 480	TAT Tyr 480	GAA Glu 480	GTC Val 480	GAA Glu 480	GTC Val 480	TGC Cys 485	TGT Cys 485	TCC Ser 485	AAC Asn 485	CTC Leu 485	AAT Asn 490	TAT Tyr 490	CTG Leu 490	AAA Lys 490	TAC Tyr 490	1536
GGA Gly 495	ATG Met 495	TTG Leu 495	ACG Thr 495	CGC Arg 495	AAA Lys 495	AAC Asn 500	AGC Ser 500	AAG Lys 500	TCC Ser 500	GCG Ala 505	ATG Met 505	CAG Gln 505	GCA Ala 505	GGA Gly 505	GAA Glu 505	1584
AGC Ser 510	AGT Ser 510	AGT Ser 510	CAA Gln 510	GCT Ala 515	GAT Asp 515	GCT Ala 515	AAA Lys 515	ACG Thr 515	GAA Glu 520	CAA Gln 520	GTT Val 520	GGA Gly 520	CAA Gln 520	AGT Ser 520	ATG Met 520	1632
TTC Phe 525	CTC Leu 525	CAA Gln 525	GGC Gly 525	GAG Glu 530	CGC Arg 530	ACC Thr 530	GAT Asp 530	GAA Glu 535	AAA Lys 535	GAG Glu 535	ATT Ile 535	CCA Pro 535	AGC Ser 535	GAG Glu 540	CAA Gln 540	1680
AAC Asn 545	ATC Ile 545	GTT Val 545	TAT Tyr 545	CGG Arg 545	GGG Gly 545	TCT Ser 550	TGG Trp 550	TAC Tyr 550	GGG Gly 550	CAT His 550	ATT Ile 555	GCC Ala 555	AGC Ser 555	AGC Ser 555	ACA Thr 555	1728
AGC Ser 560	TGG Trp 560	AGC Ser 560	GGC Gly 560	AAT Asn 560	GCT Ala 565	TCT Ser 565	GAT Asp 565	AAA Lys 565	GAG Glu 565	GGC Gly 570	GGC Gly 570	AAC Asn 570	AGG Arg 570	GCG Ala 570	GAA Glu 570	1776
TTT Phe 575	ACT Thr 575	GTG Val 575	AAT Asn 575	TTT Phe 575	GGC Gly 580	GAG Glu 580	AAA Lys 580	AAA Lys 580	ATT Ile 585	ACC Thr 585	GGC Gly 585	ACG Thr 585	TTA Leu 585	ACC Thr 585	GCT Ala 585	1824
GAA Glu 590	AAC Asn 590	AGG Arg 590	CAG Gln 590	GAG Glu 595	GCA Ala 595	ACC Thr 595	TTT Phe 595	ACC Thr 595	ATT Ile 600	GAT Asp 600	GGT Gly 600	AAG Lys 600	ATT Ile 600	GAG Glu 600	GGC Gly 600	1872
AAC Asn 605	GGT Gly 605	TTT Phe 605	TCC Ser 605	GGT Gly 610	ACG Thr 610	GCA Ala 610	AAA Lys 610	ACT Thr 610	GCT Ala 615	GAA Glu 615	TTA Leu 615	GGT Gly 615	TTT Phe 615	GAT Asp 620	CTC Leu 620	1920
GAT Asp 625	CAA Gln 625	AAA Lys 625	AAT Asn 625	ACC Thr 625	ACC Thr 625	CGC Arg 630	ACG Thr 630	CCT Pro 630	AAG Lys 630	GCA Ala 630	TAT Tyr 635	ATC Ile 635	ACA Thr 635	GAT Asp 635	GCC Ala 635	1968

AAG GTG CAG GGC GGT TTT TAC GGG CCC AAA GCC GAA GAG TTG GGC GGA	2016
Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly	
640 645 650	
TGG TTT GCC TAT CAG GGC GAT AAA CAA ACG GAA AAT ACA ACA GTT GCA	2064
Trp Phe Ala Tyr Gln Gly Asp Lys Gln Thr Glu Asn Thr Thr Val Ala	
655 660 665	
TCC GGC AAT GGA AAT TCA GCA AGC AGT GCA ACT GTC GTA TTC GGT GCG	2112
Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala	
670 675 680	
AAA CGC CAA AAG CCT GTG CAA TAAAGTAAAA	2143
Lys Arg Gln Lys Pro Val Gln	
685 690	

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

6' overl.

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	
-20 -15 -10 -5	
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser	
1 5 10	
Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser	
15 20 25	
Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala	
30 35 40	
Met Arg Leu Lys Arg Arg Asn Arg His Pro Gln Ala Lys Glu Asp Lys	
45 50 55 60	
Val Glu Leu Asn Pro Asn Asp Trp Glu Glu Thr Gly Leu Pro Ser Lys	
65 70 75	
Pro Gln Asn Leu Pro Glu Arg Gln Gln Ser Val Ile Asp Lys Val Lys	
80 85 90	
Thr Asp Asp Gly Ser Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser	
95 100 105	
Asn His Gln Asn Gly Ser Thr Asn Ser Gly Ala Asn Gln Pro Lys Asn	
110 115 120	